

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 ; Search time 25 Seconds
(Without alignments)
29.863 Million cell updates/sec

Title: US-10-006-190-1_COPY_6_23
Perfect score: 88
Sequence: 1 RLRAVIMGAPGSGKGTV.18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	226	1 KAD3_HUMAN	Q9U1J7 homo sapien
2	84	95.5	226	1 KAD3_BOVIN	P08760 bos taurus
3	84	95.5	226	1 KAD3_RAT	P29414 ratu
4	77	87.5	223	1 KAD4_HUMAN	P27144 homo sapien
5	77	87.5	223	1 KAD4_MOUSE	Q6WU9 mus musculu
6	77	87.5	223	1 KAD4_RAT	Q6WU9 mus musculu
7	75	85.2	219	1 KAD3_MOUSE	Q6WU9 mus musculu
8	62	70.5	214	1 KAD2_MOUSE	Q6WU9 mus musculu
9	62	70.5	214	1 KAD2_MOUSE	Q6WU9 mus musculu
10	61	69.3	253	1 KAD2_MOUSE	Q6WU9 mus musculu
11	61	69.3	253	1 KAD2_MOUSE	Q6WU9 mus musculu
12	60	68.2	215	1 KAD_PSEAE	Q9HXY4 pseudomonas
13	60	68.2	216	1 KAD_PSEAE	Q9HXY4 pseudomonas
14	60	68.2	216	1 KAD_PSEAE	Q9HXY4 pseudomonas
15	60	68.2	216	1 KAD_PSEAE	Q9HXY4 pseudomonas
16	60	68.2	216	1 KAD_PSEAE	Q9HXY4 pseudomonas
17	60	68.2	216	1 KAD_PSEAE	Q9HXY4 pseudomonas
18	60	68.2	216	1 KAD_PSEAE	Q9HXY4 pseudomonas
19	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
20	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
21	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
22	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
23	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
24	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
25	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
26	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
27	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
28	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
29	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
30	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
31	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
32	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas
33	59	67.0	214	1 KAD_VIBCH	Q9HXY4 pseudomonas

34	56	63.6	214	1 KAD_HAETN	P24323 haemophilus
35	56	63.6	214	1 KAD_PASMU	P57837 pasteurella
36	55	62.5	181	1 KAD_CORGL	P49973 corynebacte
37	55	62.5	215	1 KAD_LISTIN	O927M8 listeria in
38	55	62.5	215	1 KAD_LISTIN	O927M8 listeria in
39	55	62.5	215	1 KAD_LISTIN	O927M8 listeria in
40	54	61.4	36	1 KAD_STRSC	P43417 streptomyce
41	54	61.4	70	1 KAD_STRSC	P43417 streptomyce
42	54	61.4	176	1 AROK_MYCTU	P95014 mycobacteri
43	54	61.4	185	1 KAD1_SYNK3	P73302 synecocyst
44	54	61.4	194	1 KAD1_SYNK3	O8YH19 druceella me
45	54	61.4	198	1 KAD1_SYNK3	O8YH19 druceella me

ALIGNMENTS

RESULT 1	KAD3_HUMAN	STANDARD;	PRT;	226 AA.
ID	Q9U1J7			
AC	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DR	GRP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3) (AK3-alpha).			
GN	AK3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Noma T.;			
RL	submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.			
CC	-1- SUBUNIT: MONOMER (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).			
CC	-1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; AB021870; BAA87913.1; -			
DR	HSSP; P08760; 2AK3.			
DR	InterPro; IPR000850; Adenylate_kin.			
DR	Pfam; PF00406; adenylatekinase; 1.			
DR	PRINTS; PR00094; ADENYLTKINASE.			
DR	PRODOM; PD000657; Adenylate_kin; 1.			
DR	PROSITE; PS00113; ADENYLATE_KINASE; 1.			
KW	Transferase; Kinase; GTP-binding; Mitochondrion.			
FT	INT_MET 0			
FT	NP_BIND 13 21			
FT	SEQUENCE 226 AA; 25507 MW; 9F623E32A95B20C3 CRC64;			
QY	1 RLRAVIMGAPGSGKGTV 18			
DB	5 RLRAVIMGAPGSGKGTV 22			
Query Match	100.0%;	Score 88;	DB 1;	Length 226;
Best Local Similarity	100.0%;	Pred. No. 9.5e-06;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
RESULT 2	KAD3_BOVIN	STANDARD;	PRT;	226 AA.
ID	KAD3_BOVIN			

AC P08760;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3).
 GN AK3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90037053; PubMed=2478555;
 RA Yamada M., Shahjahan M., Tanabe T., Kishi F., Nakazawa A.;
 RT "Cloning and characterization of cDNA for mitochondrial GTP:AMP
 RT phosphotransferase of bovine liver.";
 RT J. Biol. Chem. 264:19192-19199(1989).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=86248102; PubMed=3013690;
 RA Tomasselli A.G., Frank R., Schiltz E.;
 RT "The complete primary structure of GTP:AMP phosphotransferase from
 RT beef heart mitochondria.";
 RT FEBS Lett. 202:303-308(1986).
 RN [3]
 RP SEQUENCE OF 1-49 FROM N.A.
 RX MEDLINE=92084124; PubMed=1748300;
 RA Shahjahan M., Yamada M., Tanaka H., Nakazawa A.;
 RT "Cloning and characterization of the gene encoding bovine
 RT mitochondrial adenylate kinase isozyme 3.";
 RT Gene 107:313-317(1991).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=91084487; PubMed=2175649;
 RA Diederichs K., Schulz G.E.;
 RT "Three-dimensional structure of the complex between the mitochondrial
 RT matrix adenylate kinase and its substrate AMP.";
 RT Biochemistry 29:8138-8144(1990).
 RL [5]
 RN X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
 RP MEDLINE=91132661; PubMed=1994037;
 RA Diederichs K., Schulz G.E.;
 RT "The refined structure of the complex between adenylate kinase from
 RT beef heart mitochondria and its substrate AMP at 1.85-A
 RT resolution.";
 RT J. Mol. Biol. 217:541-549(1991).
 RL J. Mol. Biol. 217:541-549(1991).
 CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; D10376; BAA01210.1; -
 DR EMBL; D10373; BAA01210.1; JOINED.
 DR EMBL; D10374; BAA01210.1; JOINED.
 DR EMBL; D10375; BAA01210.1; JOINED.
 DR EMBL; M25757; AAA30705.1; -
 DR PIR; A24201; A24201.
 DR PIR; A34442; A34442.
 DR PIR; JH0512; JH0512.
 DR PDB; 2AK3; 12-MAY-95.
 DR InterPro: IPR000850; Adenylate_kin.
 DR Pfam: PF00406; adenylatekinase; 1.
 DR PRINTS; PR00094; ADENYLTKINASE.

DR ProDom: PD000657; Adenylate_kin; 1.
 DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
 KW Transferase; Kinase; GTP-binding; Mitochondrion; 3D-structure.
 FT INIT_MET 0
 FT NP_BIND 13 21
 FT STRAND 10 10
 FT STRAND 8 12
 FT TURN 15 16
 FT TURN 19 19
 FT HELIX 33 36
 FT STRAND 37 45
 FT HELIX 37 45
 FT TURN 46 48
 FT TURN 50 60
 FT TURN 61 62
 FT HELIX 67 79
 FT TURN 80 81
 FT STRAND 86 89
 FT HELIX 95 102
 FT TURN 103 104
 FT STRAND 109 114
 FT STRAND 117 124
 FT HELIX 125 125
 FT STRAND 127 130
 FT TURN 131 134
 FT STRAND 135 138
 FT TURN 139 141
 FT STRAND 142 142
 FT TURN 147 148
 FT STRAND 149 149
 FT TURN 151 153
 FT STRAND 156 156
 FT STRAND 158 158
 FT TURN 161 162
 FT HELIX 165 189
 FT TURN 190 190
 FT STRAND 192 196
 FT HELIX 200 212
 FT TURN 213 214
 SQ SEQUENCE 226 AA; 25540 MW; 2B74C2FBAAA7CBA9 CRC64;
 Query Match 95.5%; Score 84; DB 1; Length 226;
 Best Local Similarity 94.4%; Pred. No. 3; 5e-05;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RLRAVIMGAPSGSGKTV 18
 DB 5 RLRAAIMGAPSGSGKTV 22
 ID KAD3_RAT STANDARD; PRT; 226 AA.
 AC P29411;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3).
 GN AK3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93224500; PubMed=8468325;
 RA Tanabe T., Yamada M., Noma T., Kajit T., Nakazawa A.;
 RT "Tissue-specific and developmentally regulated expression of the
 RT gene encoding adenylate kinase isozymes.";
 RL J. Biochem. 113:200-207(1993).
 CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

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CC -----
DR EMBL: D13062; BAA02379.1; -
DR PIR: J01945; J01945.
DR HSSP: P08760; 2AK3.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase. 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
DR Transferrase; Kinase; GTP-binding; Mitochondrion.
DR INIT_MET 0 21 BY SIMILARITY.
DR NP_BIND 13 21 GTP (BY SIMILARITY).
SQ SEQUENCE 226 AA; 25307 MW; D57FF37404AA6625 CRC64;

Query Match
Best Local Similarity 95.5%; Score 84; DB 1; Length 226;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVINGAPSGKGT 17
Db 5 RLRAVINGAPSGKGT 21

RESULT 4
KADA_HUMAN
ID KADA_HUMAN STANDARD; PRT; 223 AA.
AC P27144;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).
DE AK4 OR AK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RX MEDLINE=92347846; PubMed=1639383;
RA Xu G., O'Connell P., Stevens J., White R.;
RT "Characterization of human adenylate kinase 3 (AK3) cDNA and mapping
RT of the AK3 pseudogene to an intron of the NFI gene.";
RL Genomics 13:537-542(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: TO THE ADENYLATE KINASE FAMILY.
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CC -----
DR EMBL: X60673; CAA43088.1; -
DR EMBL: BC016180; AAH16180.1; -
DR PIR: S16381; S16381.

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DR PIR: S16380; S16380.
DR PIR: A42820; A42820.
DR HSSP: P08760; 2AK3.
DR Genew; HGNC:363; AK3.
DR MIM: 103030; -
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase. 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
DR Transferrase; Kinase; GTP-binding; Mitochondrion.
DR INIT_MET 12 20 GTP (BY SIMILARITY).
DR NP_BIND 12 20 GTP (BY SIMILARITY).
SQ SEQUENCE 223 AA; 25268 MW; 653341A8B3BC723 CRC64;

Query Match
Best Local Similarity 87.5%; Score 77; DB 1; Length 223;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RLRAVINGAPSGKGT 18
Db 4 RLRAVINGAPSGKGT 21

RESULT 5
KADA_MOUSE
ID KADA_MOUSE STANDARD; PRT; 223 AA.
AC Q9WUR9; Q9R1X7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).
DE AK4 OR AK-4 OR AK3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RX MEDLINE=99033072; PubMed=9813319;
RA Yoneda T., Sato M., Maeda M., Takagi H.;
RT "Identification of a novel adenylate kinase system in the brain:
RT cloning of the fourth adenylate kinase".
RL Brain Res. Mol. Brain Res. 62:187-195(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Noma T.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE PYRAMIDAL CELLS IN THE
CC HIPPOCAMPUS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM IN A
CC REGION-SPECIFIC MANNER FROM THE MIDDLE STAGE OF EMBRYOGENESIS TO
CC THE ADULTHOOD IN THE RODENT.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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CC -----
DR EMBL: D85036; BAA77760.1; -
DR EMBL: AB020239; BAA77363.1; -
DR HSSP: P08760; 2AK3.
DR MGD; MGI:87980; AK4.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase. 1.
DR PRINTS: PR00094; ADENYLTKINASE.

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DR ProDom: PD000657; Adenylate_kin; 1.
 DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
 KM Transferase; Kinase; GTP-binding; Mitochondrion.
 FT NP_BIND 12 20 GTP (BY SIMILARITY).
 FT CONFLICT 68 68 V -> A (IN REF. 2).
 FT CONFLICT 187 187 S -> N (IN REF. 2).
 FT CONFLICT 190 190 V -> M (IN REF. 2).
 SQ SEQUENCE 223 AA; 250522949715155EC CRC64;
 Query Match 87.5%; Score 77; DB 1; Length 223;
 Best Local Similarity 83.3%; Pred. No. 0.00035;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RLRAVIMGAGSGKGV 18
 Db 4 KILRAVILGPPGSGKGV 21
 RESULT 6
 KAD4_RAT ID KAD4_RAT STANDARD; PRT; 223 AA.
 AC Q9WUS0;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP
 transphosphorylase).
 GN AK4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistar; TISSUE=Forebrain;
 RX MEDLINE=99033072; PubMed=9813319;
 RA Yoneda T., Sato M., Maeda M., Takagi H.;
 RT "Identification of a novel adenylate kinase system in the brain:
 cloning of the fourth adenylate kinase.";
 RL Brain Res. Mol. Brain Res. 62:187-195(1998).
 CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE PRADMD CELLS IN THE
 HIPPOCAMPUS.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM IN A
 REGION-SPECIFIC MANNER FROM THE MIDDLE STAGE OF EMBRYOGENESIS TO
 THE ADULTHOOD IN THE RODENT.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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 CC -----
 CC EMBL: D87809; BAA77761.1; -
 DR HSSP: P08760; ZAK3.
 DR InterPro: IPR000850; Adenylate_kin.
 DR Pfam: PF00406; adenylatekinase; 1.
 DR PRINTS: PR00094; ADENYLTKINASE.
 DR PRODOM: PD000657; Adenylate_kin; 1.
 DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
 KM Transferase; Kinase; GTP-binding; Mitochondrion.
 FT NP_BIND 12 20 GTP (BY SIMILARITY).
 SQ SEQUENCE 223 AA; 25203 MW; B5A9BE43CF3C19B CRC64;
 Query Match 87.5%; Score 77; DB 1; Length 223;
 Best Local Similarity 83.3%; Pred. No. 0.00035;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RLRAVIMGAGSGKGV 18
 Db 4 KILRAVILGPPGSGKGV 21

Db 4 KILRAVILGPPGSGKGV 21
 RESULT 7
 KAD3_MOUSE ID KAD3_MOUSE STANDARD; PRT; 219 AA.
 AC Q9WTP7;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3)
 DE (Fragment).
 GN AK3 OR AK-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Noma T.;
 CC Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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 CC -----
 CC EMBL: AB020203; BAA77360.1; -
 DR HSSP: P08760; ZAK3.
 DR MGD: MGI:87979; AK3.
 DR InterPro: IPR000850; Adenylate_kin.
 DR Pfam: PF00406; adenylatekinase; 1.
 DR PRINTS: PR00094; ADENYLTKINASE.
 DR PRODOM: PD000657; Adenylate_kin; 1.
 KM Transferase; Kinase; GTP-binding; Mitochondrion.
 FT NP_BIND 1 14 GTP (BY SIMILARITY).
 SQ SEQUENCE 219 AA; 24640 MW; 7DDB8DF2C0E87C5 CRC64;
 Query Match 85.2%; Score 75; DB 1; Length 219;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 RAVIMGAGSGKGV 18
 Db 1 RAVIMGAGSGKGV 15
 RESULT 8
 KAD_MYCGA ID KAD_MYCGA STANDARD; PRT; 214 AA.
 AC O52352;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
 GN ADK.
 OS Mycoplasma gallisepticum.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A5969Var.B;
 RA Skamrov A., Feoktistova E., Goldman M., Beabealashvili R.;

```

RT      "Cloning and sequencing of Mycoplasma gallisepticum chromosome region
RT      containing opsrons s10 and rnz35."
RT      Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
RL      FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC      MAINTENANCE AND CELL GROWTH.
CC      -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC      -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC      -----
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CC      -----
DR      EMBL; AF036708; AAB95407.1; -.
DR      HSSP; P08760; 2AK3.
DR      InterPro: IPR000850; Adenylate_kin.
DR      Pfam; PF00406; adenylatekinase.1.
DR      PRINTS; PR00094; ADENYLTKINASE.
DR      PRODOM; PD000657; Adenylate_kin.1.
DR      PROSITE; PS00113; ADENYLATE_KINASE.1.
KW      Transferase; Kinase; ATP-binding.
FT      NP_BIND 8 16
FT      SEQUENCE 214 AA; 24962 MW; 4BA2D57B454C1C6D CRC64;

Query Match      70.5%; Score 62; DB 1; Length 214;
Best Local Similarity 52.9%; Pred. No. 0.046;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      2 LRAVIMGAPSGSGKTV 18
DB      1 MIRLIFLGAPGSGKGTI 17
      :::::|||||:::

RESULT 9
KAD2_YEAST      STANDARD; PRT; 225 AA.
AC      P26364;
DT      01-AUG-1992 (Rel. 23, Created)
DT      01-AUG-1992 (Rel. 23, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Adenylate kinase 2 (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN      ADK2 OR PAK3 OR YER170W.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX      NCBI_TaxID=4932;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92267376; PubMed=1587477;
RA      Cooper A.J., Friedberg E.C.;
RT      "A putative second adenylate kinase-encoding gene from the yeast
RT      Saccharomyces cerevisiae."
RL      Gene 114:145-148(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=DL-1;
RX      MEDLINE=92318888; PubMed=1620094;
RA      Schlicker R., Magdolen V., Bandlow W.;
RT      "A new member of the adenylate kinase family in yeast: PAK3 is highly
RT      homologous to mammalian AK3 and is targeted to mitochondria."
RL      Mol. Gen. Genet. 233:363-371(1992).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=S288C / AB972;
RA      Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA      Aviles E., Berto A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA      Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
RA      Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,

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RA      Mosedale D., Nakahara K., Nameth A., Norgren R., Oefner P., Oh C.,
RA      Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA      Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL      Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
CC      FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC      MAINTENANCE AND CELL GROWTH.
CC      -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC      -1- SUBCELLULAR LOCATION: Mitochondrial.
CC      -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC      -----
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CC      -----
DR      EMBL; M77757; AAA34418.1; -.
DR      EMBL; X65126; CAA46254.1; -.
DR      EMBL; U18922; AAB64697.1; -.
DR      PIR; JC1135; JC1135.
DR      PIR; S23568; S23568.
DR      HSSP; P08760; 2AK3.
DR      SGD; S0000972; ADK2.
DR      InterPro: IPR000850; Adenylate_kin.
DR      Pfam; PF00406; adenylatekinase.1.
DR      PRINTS; PR00094; ADENYLTKINASE.
DR      PRODOM; PD000657; Adenylate_kin.1.
DR      PROSITE; PS00113; ADENYLATE_KINASE.1.
KW      Transferase; Kinase; ATP-binding; Mitochondrion.
FT      NP_BIND 21 29
FT      SEQUENCE 225 AA; 25194 MW; 3B192BE2535BF91F CRC64;

Query Match      70.5%; Score 62; DB 1; Length 225;
Best Local Similarity 73.3%; Pred. No. 0.049;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      3 LRAVIMGAPSGSGKT 17
DB      15 LRLILGAPSGSGKT 29
      :::::|||||:::

RESULT 10
KAD_CHLTR      STANDARD; PRT; 245 AA.
AC      O84130;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN      ADK OR CT128.
OS      Chlamydia trachomatis.
OC      Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX      NCBI_TaxID=813;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99000809; PubMed=9784136;
RA      Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA      Mitchell W.P., Ollinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA      Davis R.W.;
RT      "Genome sequence of an obligate intracellular pathogen of humans:
RT      Chlamydia trachomatis."
RL      Science 282:754-759(1998).
CC      FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC      MAINTENANCE AND CELL GROWTH.
CC      -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC      -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC      -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE001286; AAC67719.1; -
DR HSSP: P08760; 2AK3.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
DR Transferrase; Kinase; ATP-binding; Complete proteome.
FT NP BIND 12 ATP (BY SIMILARITY)
SQ SEQUENCE 245 AA; 27784 MM; 3F38D306ED75D09F CRC64;

Query Match 69.3%; Score 61; DB 1; Length 245;
Best Local Similarity 91.7%; Pred. No. 0.074;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VINGAPSGSGKT 17
Db 9 IIMGAPSGSGKT 20
:|||||

RESULT 11
KAD_CHLMU STANDARD; PRT; 253 AA.
ID KAD_CHLMU
AC Q9PKR0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK OR TC0404.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOPN / Nig9;
RA MEDLINE=20150235; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gall S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utechtback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Eisen J., Fraser C.M., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RT "Genome sequences of Chlamydia trachomatis MOPN and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC -----
DR EMBL: AE002307; AAF39261.1; -
DR HSSP: P08760; 2AK3.
DR TIGR: TC0404;
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR TRANSF: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.

DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
DR Transferrase; Kinase; ATP-binding; Complete proteome.
FT NP BIND 12 ATP (BY SIMILARITY)
SQ SEQUENCE 253 AA; 28597 MM; 9F915F6ECBAF0D CRC64;

Query Match 69.3%; Score 61; DB 1; Length 253;
Best Local Similarity 91.7%; Pred. No. 0.076;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VINGAPSGSGKT 17
Db 9 IIMGAPSGSGKT 20
:|||||

RESULT 12
KAD_PSEAE STANDARD; PRT; 215 AA.
ID KAD_PSEAE
AC Q9HXA4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK OR PA3686.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RA MEDLINE=20437337; PubMed=10984043;
RA Slover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou Y.,
RA Gaber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olsen M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC -----
DR EMBL: AE004788; AAC07074.1; -
DR HSSP: P05082; 1E4V.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
DR Transferrase; Kinase; ATP-binding; Complete proteome.
FT NP BIND 15 ATP (BY SIMILARITY)
SQ SEQUENCE 215 AA; 23107 MM; 744C9FDC51E1C057 CRC64;

Query Match 68.2%; Score 60; DB 1; Length 215;
Best Local Similarity 60.0%; Pred. No. 0.09;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LRVIMGAPSGSGKT 17
Db 1 MRVILGAPGAGKT 15
:|||||

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RESULT 13
KAD_PSEPU STANDARD; PRT; 216 AA.
AC Q92409;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mt-2;
RA Takaoaka H., Miura K., Nakazawa A.;
RT "Complete adk gene from Pseudomonas putida mt-2."
RL Submitted (MAR-1999) to the EMBL/Genbank/DDIJ databases.
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC -----
CC EMBL: AB024426; BAA75818.1; -
CC DR HSSP: P05082; 1EAV.
CC DR InterPro: IPR000850; Adenylate_kin.
CC DR Pfam: PF00406; adenylatekinase; 1.
CC DR PRINTS: PR00094; ADENYLTKINASE.
CC DR ProDom: PD000657; Adenylate_kin; 1.
CC DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
CC KM Transferase; Kinase; ATP-binding.
CC FT NP_BIND 7 15 ATP (BY SIMILARITY).
CC SQ SEQUENCE 216 AA; 23222 MW; C7EC04EC62C9ECA7 CRC64;

Query Match 68.2%; Score 60; DB 1; Length 216;
Best Local Similarity 60.0%; Pred. No. 0.09;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVINGAPGSGKGT 17
DB 1 MRVILGAPGAGKGT 15

RESULT 14
KAD2_MOUSE STANDARD; PRT; 231 AA.
ID KAD2_MOUSE
AC Q9WTP6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).
GN AK2 OR AK-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Noma T.;

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RL Submitted (NOV-1998) to the EMBL/Genbank/DDIJ databases.
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial intermembrane space (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC -----
CC EMBL: AB020202; BAA77359.1; -
CC DR HSSP: P08166; 1AK2.
CC DR MGD: MGI:87978; AK2.
CC DR InterPro: IPR000850; Adenylate_kin.
CC DR Pfam: PF00406; adenylatekinase; 1.
CC DR PRINTS: PR00094; ADENYLTKINASE.
CC DR ProDom: PD000657; Adenylate_kin; 1.
CC DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
CC KM Transferase; Kinase; ATP-binding; Mitochondrion.
CC FT INIT_MET 0 0
CC FT NP_BIND 21 29 ATP (BY SIMILARITY).
CC SQ SEQUENCE 231 AA; 25693 MW; A90DA6797CFE5E1E CRC64;

Query Match 68.2%; Score 60; DB 1; Length 231;
Best Local Similarity 66.7%; Pred. No. 0.097;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVINGAPGSGKGT 17
DB 15 IRAWLGPAGKGT 29

RESULT 15
KAD2_HUMAN STANDARD; PRT; 238 AA.
ID KAD2_HUMAN
AC P54819; O16856;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).
GN AK2 OR ADK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97000211; PubMed=8843353;
RA Lee Y., Kim J.W., Lee I.A., Kang H.B., Choe Y.K., Lee H.G.,
RA Lim J.S., Kim H.J., Park C., Choe I.S.;
RT "Cloning and characterization of cDNA for human adenylate kinase 2A."
RL Biochem. Mol. Biol. Int. 39:833-842(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98162934; PubMed=9504408;
RA Lee Y., Kim J.W., Lee S.M., Kim H.J., Lee K.S., Park C., Choe I.S.;
RT "Cloning and expression of human adenylate kinase 2 isoforms:
RT differential expression of adenylate kinase 1 and 2 in human muscle
RT tissues."
RL J. Biochem. 123:47-54(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strausberg R.;

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RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC -! FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -! CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -! SUBUNIT: MONOMER (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: Mitochondrial intermembrane space.
CC -! ALTERNATIVE PRODUCTS: 2 ISOFORMS; AK2A (SHOWN HERE) AND AK2B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -! TISSUE SPECIFICITY: ABUNDANT IN HEART.
CC -! SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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CC -----
DR EMBL; U39945; AAC52061.1; -
DR EMBL; U84371; AAB41790.1; -
DR EMBL; U54645; AAC13881.1; -
DR EMBL; BC009405; AAH09405.1; -
DR HSSP; P08166; IAK2.
DR Genew; HGNC:362; AK2.
DR MIM; 103020; -
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; adenylatekinase; 1.
DR PRINTS; PRO0094; ADENYLTKINASE.
DR Prodom; PD000657; Adenylate_kin; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
DR Transferrase; Kinase; ATP-binding; Mitochondrion; Alternative splicing.
FT INIT_MET 0
FT NP_BIND 21 29 BY SIMILARITY.
FT VARSPIC 231 238 CKDLVMT -> S (IN ISOFORM AK2B).
SQ SEQUENCE 238 AA; 26346 MW; 34B3844F355EC3D1 CRC64;

Query Match 68.2%; Score 60; DB 1; Length 238;
Best Local Similarity 66.7%; Pred. No. 0.1;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVIMGAPSGAGKT 17
DB 15 IRAVILGPPGAGAGKT 29

```

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OM protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 ; Search time 43 Seconds
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40.242 Million cell updates/sec

Title: US-10-006-190-1_COPY_6_23

Perfect score: 88

Sequence: 1 RLRRAVIMGAPGSGKGTIV 18

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	95.5	227	2 J01945	nucleoside-triphos
2	84	95.5	227	2 A34442	nucleoside-triphos
3	77	87.5	223	1 K1HUA3	nucleoside-triphos
4	62	70.5	198	2 B82825	adenylate kinase x
5	62	70.5	225	2 S23568	adenylate kinase (
6	61	69.3	245	2 D71554	probable adenylate
7	61	69.3	253	2 B81706	adenylate kinase T
8	60	68.2	215	2 G83184	adenylate kinase P
9	60	68.2	232	2 JC5893	adenylate kinase
10	60	68.2	239	2 G02248	adenylate kinase (
11	60	68.2	239	2 J01944	adenylate kinase (
12	60	68.2	248	2 S44766	adenylate kinase (
13	59	67.0	214	1 K7ECA	adenylate kinase (
14	59	67.0	214	2 S70734	adenylate kinase (
15	59	67.0	214	2 C82255	adenylate kinase V
16	59	67.0	214	2 AC0378	adenylate kinase (
17	59	67.0	214	2 AC0563	adenylate kinase (
18	59	67.0	214	2 C85545	adenylate kinase (
19	59	67.0	214	2 G90694	adenylate kinase (
20	59	67.0	215	2 S61841	adenylate kinase (
21	59	67.0	215	2 S61843	adenylate kinase (
22	59	67.0	215	2 B84986	adenylate kinase (
23	59	67.0	215	2 F81154	adenylate kinase N
24	59	67.0	234	2 B29792	adenylate kinase (
25	59	67.0	241	2 J50422	adenylate kinase (
26	57	64.8	205	2 S17070	adenylate kinase (
27	56	63.6	181	2 B87138	probable adenylate
28	56	63.6	181	2 T45390	adenylate kinase (
29	56	63.6	213	2 D86521	adenylate kinase (

30	56	63.6	213	2 H72100	adenylate kinase C
31	56	63.6	214	2 I64062	adenylate kinase (
32	55	62.5	43	2 I40341	adenylate kinase (
33	55	62.5	215	2 A81777	adenylate kinases
34	55	62.5	215	2 A81401	adenylate kinases
35	54	61.4	70	2 PC4087	adenylate kinase (
36	54	61.4	176	2 G70658	probable arok prot
37	54	61.4	187	2 S77483	adenylate kinase (
38	54	61.4	194	2 AD3349	adenylate kinase (
39	54	61.4	199	2 PC4230	adenylate kinase (
40	54	61.4	205	2 S50007	adenylate kinase (
41	54	61.4	214	2 I64218	adenylate kinase (
42	54	61.4	218	2 S43016	adenylate kinase (
43	54	61.4	222	1 K1BYA	adenylate kinase (
44	53	60.2	177	2 H97205	probable kinase fr
45	53	60.2	181	2 H70822	probable adenylate

ALIGNMENTS

RESULT 1

J01945

nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3, mitochondrial - rat

N:Alternate names: GTP-AMP phosphotransferase AK3

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002

C:Accession: J01945

R:Tanabe, T.; Yamada, M.; Noma, T.; Kajii, T.; Nakazawa, A.

J. Biochem. 113, 200-207, 1993

A:Title: Tissue-specific and developmentally regulated expression of the genes encodi

A:Reference number: P00534; MUID:93224500; PMID:8468325

A:Accession: J01945

A:Molecule type: mRNA

A:Residues: 1-227 <TAN>

A:Cross-references: DDBJ:D13062; NID:q220797; PIDN:BA02379.1; PID:q450312

A:Superfamily: adenylate kinase

K:Keywords: ATP; GTP; mitochondrion; nucleotide binding; P-loop; phosphotransferase

F:14-21/Region: nucleotide-binding motif A (P-loop)

Query Match

Best Local Similarity 95.5%; Score 84; DB 2; Length 227;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLRRAVIMGAPGSGKGT 17

Db 6 RLRRAVIMGAPGSGKGT 22

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FEBS Lett. 202,303-308, 1986
A:Title: The complete primary structure of GMP:AMP phosphotransferase from beef heart m
A:Reference number: A24201, MUID:86248102, PMID:3013690
A:Accession: A24201..
A:Molecule type: protein
A:Residues: 2-10,12-227 <TOM>
C:Genetics:
A:Gene: AK3
A:Introns: 51/1; 91/1; 148/3; 188/2
C:Superfamily: adenylate kinase
C:Keywords: ATP: mitochondrion; nucleotide binding; P-loop; phosphotransferase
P:2-227/Product: GTP-AMP phosphotransferase, mitochondrial #status predicted <MAT>
F:14-21/Region: nucleotide-binding motif A (P-loop)

Query Match          95.5%; Score 84; DB 2; Length 227;
Best Local Similarity 94.4%; Pred. No. 0.00012;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  RLRLAIVINGAPGSGSGKTIV 18
        ||||| ||||| |||||
DB       6  RLRLAIVINGAPGSGSGKTIV 23

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RESULT 3
KIHUA3
nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3 - human
N:Alternate names: adenylylate kinase 3
C:Species: Homo sapiens (man)
C:/Date: 17-Apr-1993 #sequence_revision 23-Mar-1995 #text_change 03-Jun-2002
C:/Accession: M42820; S16380; S16381
R:Xu, G.; O'Connell, P.; Stevens, J.; White, R.
Genomics 13, 537-542, 1992
A:/Title: Characterization of human adenylylate kinase 3 (AK3) cDNA and mapping of the AK3
A:/Reference number: A42820; MUID:92347846; PMID:1639383
A:/Accession: A42820
A:/Molecule type: mRNA
A:/Residues: 1-223 <XUG>
A:/Cross-references: EMBL:X60673; NID:g28576; PIDN:CAA43088.1; PID:g28577; GB:S41502
A:/Experimental source: frontal.cortex
A:/Note: sequence extracted from NCBI backbone (NCBIN:109644, NCBIP:109645)
C:/Comment: This Isozyme is found in the mitochondrial matrix.
C:/Geneclis:
A:/Gene: GDB:AK3
A:/Cross-references: GDB:118988; OMIM:103030
A:/Map position: 9pter-pJ3
C:/Function:
A:/Description: catalyzes the reversible phosphorylation of adenine monophosphate with nu
A:/Note: GTP is preferred to ATP as a substrate
C:/Superfamily: adenylylate kinase
C:/Keywords: ATP; mitochondrial matrix; mitochondrion; P-loop; phosphotransferase
F:12-19/Region: nucleotide-binding motif A (P-loop) #status atypical
F:85-89/Region: nucleotide-binding motif B #status atypical
F:22,33,35,88/Active site: Cys, His, Ser, Asp #status predicted

Query Match      87.5%; Score 77; DB 1; Length 223;
Best Local Similarity 83.3%, Pred. No. 0.0012;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RLRAVINGAGSGSGKGT V 18
          :| | | | | | | | | | | | |
Db       4 KLRRAVILGPDSGKGV T 21

RESULT 4
B82825
adenylylate kinase XF0275 [imported] - Xylella fastidiosa (strain 9a5c)
C:/Species: Xylella fastidiosa
C:/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:/Accession: B82825
R:anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
A:/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:/Reference number: A82515; MUID:20365717; PMID:10910347

```

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: B82875
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-198 <STM>
A:Cross-references: GB:AEO03881; GB:AEO03849; NID:G9105093; PIDN:AAF83088.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briões, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier
as-Neto, E.; Docena, C.; El-Dorrry, H.; Fachinani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Perito, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0275
C:Superfamily: adenylate kinase

	Query Match	70.5%	Score 62;	DB 2;	Length 198;
	Best Local Similarity	68.8%	Pred. No. 0.13;		
	Matches 11; Conservative		3; Mismatches	2; Indels	0; Gaps

Oy 2 LLRAVINGAPSGKGT 17
| : | : | : | : | : | : |
Db 11 LMRLVLGPPOSGKGT 26

RESULT 5
S23568
adenylylate kinase (EC 2.7.4.3) ADK2 - yeast (Saccharomyces cerevisiae)
N:Alternate names: PAK3 protein; protein YER170w
C:Species: Saccharomyces cerevisiae
C:Date: 12-Mar-1993 #sequence,revision 12-Mar-1993 #text_change 19-Jan-2001
A:Accession: S23568; JCI135; S50673
R:Schricker, R.; Magdolen, V.; Bandlow, W.
MOL. Genet. 233, 363-371, 1992
A:Title: A new member of the adenylylate kinase family in yeast: PAK3 is highly homologous to the yeast PAK3 protein
A:Reference number: S23568; MUID:92318888; PMID:1620094
A:Accession: S23568
A:Molecule type: DNA
A:Residues: 1-225 <SOCH>
A:Cross-references: EMBL:X65126; NID:g14096; PIDN:CAA6254.1; PID:g44097
R:Cooper, A.J.; Friedberg, E.C.
Gene 114, 145-148, 1992
A:Title: A putative second adenylylate kinase-encoding gene from the yeast Saccharomyces cerevisiae
A:Reference number: JCI135; MUID:92267376; PMID:1567477
A:Accession: JCI135
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-225 <COO>
A:Cross-references: GB:M77757; NID:g171045; PIDN:AAA34418.1; PID:g171046
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 9163 and 9132.
A:Reference number: S50673
A:Accession: S50673
A:Molecule type: DNA
A:Residues: 1-225 <DIE>
A:Cross-references: EMBL:U18922; NID:g603405; PIDN:AMB64697.1; PID:g603411; MIPS:YER1
C:Genetics:
A:Gene: SGD:ADK2; PAK3
A:Cross-references: SGD:S0000972; MIPS:YER170w
A:Map position: 5R
C:Function:
A:Description: phosphotransferase
A:Superfamily: adenylylate kinase

C:Keywords: ATP; mitochondrion; nucleotide binding; P-loop; phosphotransferase
F:21-28/Region: nucleotide-binding motif A (P-loop)

Query Match 70.5%; Score 62; DB 2; Length 225;
Best Local Similarity 73.3%; Pred. No. 0.15;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 LRAVINGAPGSGKGT 17
|| :|||:|||||
DB 15 LRLLLGAPGSGKGT 29

RESULT 6
D71554
probable adenylate cyclase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 24-Nov-1999
C:Accession: D71554

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; MUID:99000809; PMID:9784136

A:Accession: D71554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <ARN>
A:Cross-references: GB:AE001286; GB:AE001273; NID:g33228516; PIDN:AA67719.1; PID:g3322852
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: adk
C:Superfamily: adenylate kinase

Query Match 69.3%; Score 61; DB 2; Length 245;
Best Local Similarity 91.7%; Pred. No. 0.23;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 VINGAPGSGKGT 17
:|||||
DB 9 IIMGAPGSGKGT 20

RESULT 7
B81706
adenylate kinase TC0404 [Imported] - Chlamydia muridarum (strain N19g)
C:Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000
C:Accession: B81706

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935

A:Accession: B81706
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <TEP>
A:Cross-references: GB:AE002307; GB:AE002160; NID:g7190442; PIDN:AAF39261.1; PID:g719044
A:Experimental source: strain N19g (Mopn)
C:Genetics:
A:Gene: TC0404
C:Superfamily: adenylate kinase

Query Match 69.3%; Score 61; DB 2; Length 253;
Best Local Similarity 91.7%; Pred. No. 0.23;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 VINGAPGSGKGT 17
:|||||
DB 9 IIMGAPGSGKGT 20

RESULT 8
G83184

adenylate kinase PA3686 [Imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83184

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: G83184
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-215 <STO>
A:Cross-references: GB:AE004788; GB:AE004091; NID:g9949846; PIDN:AA607074.1; GSPDB:GNI
A:Experimental source: strain PA01
C:Genetics:
A:Gene: adk; PA3686
C:Superfamily: adenylate kinase

Query Match 68.2%; Score 60; DB 2; Length 215;
Best Local Similarity 60.0%; Pred. No. 0.27;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 LRAVINGAPGSGKGT 17
:|||||
DB 1 MRVILGAPGAGKGT 15

RESULT 9
JC5893
adenylate kinase (EC 2.7.4.3) 2B - human
N:Alternate names: ATP-AMP transphosphorylase
C:Species: Homo sapiens (man)
C:Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 18-Jun-1999
C:Accession: JC5893

R:Lee, Y.; Kim, J.W.; Lee, S.M.; Kim, H.J.; Lee, K.S.; Park, C.; Choe, I.S. J. Biochem. 123, 47-54, 1998
A:Title: Cloning and expression of human adenylate kinase 2 isozymes: Differential expression of human adenylate kinase 2 isozymes: Differential expression
A:Reference number: JC5893; MUID:98162934; PMID:9504408
A:Accession: JC5893
A:Molecule type: mRNA
A:Residues: 1-232 <LEP>
A:Cross-references: GB:U54645; NID:g1710886; PIDN:AA13881.1; PID:g1477653
A:Experimental source: tissue fetal liver
C:Comment: This key enzyme is involved in energy metabolism.
C:Genetics:
A:Gene: adk2b
C:Function:

A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
A:Note: magnesium required
C:Superfamily: adenylate kinase
C:Keywords: alternative splicing; ATP; P-loop; phosphotransferase
F:22-29/Region: nucleotide-binding motif A (P-loop) #status atypical
F:95-100/Region: nucleotide-binding motif B #status atypical
F:42-92/Dsulfide bonds: #status predicted
F:43,99,145/Active site: His, Asp, His #status predicted

Query Match 68.2%; Score 60; DB 2; Length 232;
Best Local Similarity 66.7%; Pred. No. 0.3;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 LRAVINGAPGSGKGT 17
:|||||
DB 16 IRAVLLGPGAGKGT 30

RESULT 10
G02248
adenylate kinase (EC 2.7.4.3) 2 - human
N:Alternate names: ATP-AMP transphosphorylase
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 18-Jun-1999

C:Accession: G02248
 R:Choe, I.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: H00907
 A:Accession: G02248
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-239 <CHO>
 A:Cross-references: EMBL:U39945; NID:g1209686; PIDN:ANC52061.1; PID:g1209687
 A:Experimental source: tissue fetal liver
 C:Genetics:
 A:Gene: adk2
 C:Function:
 A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
 A:Note: magnesium required
 C:Superfamily: adenylate kinase
 C:Keywords: alternate splicing; ATP; P-loop; phosphotransferase
 F:22-29/Region: nucleotide-binding motif A (P-loop) #status atypical
 F:95-100/Region: nucleotide-binding motif B #status atypical
 F:42-92/Disulfide bonds: #status predicted
 F:43,99,145/Active site: His, Asp, His #status predicted

Query Match 68.2%; Score 60; DB 2; Length 239;
 Best Local Similarity 66.7%; Pred. No. 0.31;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 LRAVIMGAPSGSGKT 17
 :|||:|11:||||
 Db 16 IRAWLGPFGAGKGT 30

RESULT 11
 J01944
 adenylate kinase (EC 2.7.4.3) 2, mitochondrial - rat
 N:Alternate names: ATP-AMP phosphotransferase AK2
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-Feb-1994 #sequence, revision 03-Feb-1994 #text_change 20-Jun-2000
 C:Accession: J01944
 R:Tanabe, T.; Yamada, M.; Noma, T.; Kajii, T.; Nakazawa, A.
 J. Biochem. 113, 200-207, 1993
 A:Title: Tissue-specific and developmentally regulated expression of the genes encoding
 A:Reference number: F00534; MUID:93224500; PMID:8468325
 A:Accession: J01944
 A:Molecule type: mRNA
 A:Residues: 1-239 <TRAN>
 A:Cross-references: DDBJ:DJ3061; NID:g220795; PIDN:BA02378.1; PID:g220796
 C:Function:
 A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
 A:Note: magnesium required
 C:Superfamily: adenylate kinase
 C:Keywords: ATP; mitochondrion; P-loop; phosphotransferase
 F:22-29/Region: nucleotide-binding motif A (P-loop) #status atypical
 F:95-100/Region: nucleotide-binding motif B #status atypical
 F:42-92/Disulfide bonds: #status predicted
 F:43,99,145/Active site: His, Asp, His #status predicted

Query Match 68.2%; Score 60; DB 2; Length 239;
 Best Local Similarity 66.7%; Pred. No. 0.31;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 LRAVIMGAPSGSGKT 17
 :|||:|11:||||
 Db 16 IRAWLGPFGAGKGT 30

RESULT 12
 S44766
 adenylate kinase (EC 2.7.4.3) - Caenorhabditis elegans
 N:Alternate names: ATP-AMP transphosphorylase; protein C29E4.8
 C:Species: Caenorhabditis elegans
 C:Date: 14-Sep-1994 #sequence, revision 12-May-1995 #text_change 23-Mar-2001
 C:Accession: S44766
 R:Wilsson, R.

submitted to the EMBL Data Library, September 1993
 A:Description: Sequence of the C. elegans cosmid C29E4.
 A:Reference number: S44738
 A:Accession: S44766
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-248 <WIL>
 A:Cross-references: EMBL:L23651; NID:g388575; PIDN:AAA27957.1; PID:g388577
 C:Genetics:
 A:Insertions: 58/1; 121/3; 204/3
 C:Function:
 A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
 A:Note: magnesium required
 C:Superfamily: adenylate kinase
 C:Keywords: ATP; P-loop; phosphotransferase
 F:33-40/Region: nucleotide-binding motif A (P-loop) #status atypical
 F:106-111/Region: nucleotide-binding motif B #status atypical
 F:53-103/Disulfide bonds: #status predicted
 F:54,110,156/Active site: His, Asp, His #status predicted

Query Match 68.2%; Score 60; DB 2; Length 248;
 Best Local Similarity 64.7%; Pred. No. 0.32;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGSGKT 17
 :|||:|11:||||
 Db 25 RGRATFGPFGSGKGT 41

RESULT 13
 K1ECA
 adenylate kinase (EC 2.7.4.3) [validated] - Escherichia coli (strain K-12)

N:Alternate names: ATP-AMP transphosphorylase
 C:Species: Escherichia coli
 C:Date: 31-Mar-1988 #sequence, revision 31-Mar-1988 #text_change 01-Mar-2002
 C:Accession: A24275; S25734; A64778
 R:Brune, M.; Schumann, R.; Wittinghofer, F.
 Nucleic Acids Res. 13, 7139-7151, 1985
 A:Title: Cloning and sequencing of the adenylate kinase gene (adk) of Escherichia coli
 A:Reference number: A24275; MUID:86041903; PMID:2997739
 A:Accession: A24275
 A:Molecule type: DNA
 A:Residues: 1-214 <BRU>
 A:Cross-references: GB:X03038; NID:g40903; PIDN:CAA26840.1; PID:g40904
 A:Experimental source: K-12
 R:Myamoto, K.; Nakahigashi, K.; Nishimura, K.; Imokuchi, H.
 J. Mol. Biol. 219, 393-398, 1991
 A:Title: Isolation and characterization of visible light-sensitive mutants of Escheri
 A:Reference number: S16118; MUID:91269316; PMID:2051480
 A:Accession: S25734
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 108-214 <MY>
 A:Cross-references: EMBL:D90259; NID:g285768; PIDN:BA014303.1; PID:g216516
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.: Rose, D.J.; Mau, B.; Shaoh, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: A64778
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-214 <BLAT>
 A:Cross-references: GB:AE000153; GB:U00096; NID:g1786671; PIDN:ANC73576.1; PID:g17866
 A:Experimental source: strain K-12, substrain MG1655
 R:Rose, T.; Brune, M.; Wittinghofer, A.; Le Bley, K.; Surewicz, W.K.; Mantsch, H.H.;
 J. Biol. Chem. 266, 10781-10786, 1991
 A:Title: Structural and catalytic properties of a deletion derivative (delta-133-157)
 A:Reference number: A40519; MUID:91250371; PMID:2040598
 A:Contents: annotation; deletion mutant characterization
 A:Note: a construct lacking residues 133-157, corresponding to the insert found in la
 Of maximum levels for wild type enzyme
 R:Berry, M.B.; Meador, B.; Bolderback, T.; Liang, P.; Glaser, M.; Phillips Jr., G.N.

submitted to the Brookhaven Protein Data Bank, February 1994

A:Reference number: A52276; PDB:1ANK

A:Contents: annotation: X-ray crystallography, 2.0 angstroms, residues 1-214

C:Genetics:

A:Gene: adk; plsa; dnaW

A:Map position: 11 min

C:Function:

A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

F:80-85/Region: nucleotide-binding motif B #status atypical

F:30-84/Active site: Ser, Asp #status predicted

Query Match 67.0%; Score 59; DB 1; Length 214;

Best Local Similarity 60.0%; Pred. No. 0.38;

Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVIMGAPGSGKGT 17

DB 1 MRLILGAPGAGKGT 15

RESULT 14

S70734

adenylate kinase (EC 2.7.4.3) - Yersinia enterocolitica

N:Alternate names: ATP-AMP transphosphorylase

C:Species: Yersinia enterocolitica

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999

C:Accession: S70734; S51258

R:Skurnik, M.; Venho, R.; Tolvanen, P.; Al-Hendy, A.

Mol. Microbiol. 17, 575-594, 1995

A:Title: A novel locus of Yersinia enterocolitica serotype O:3 involved in lipopolysacch

A:Reference number: S70734; MUID:96100456; PMID:8559076

A:Accession: S70734

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-214 <SKU>

A:Cross-references: EMBL:247767; NID:9633689; PIDN:CAA87696.1; PID:9633690

A:Experimental source: strain 6471/76 serotype O:3

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

C:Genetics:

A:Gene: adk

C:Function:

A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

F:80-85/Region: nucleotide-binding motif B #status atypical

F:126/Active site: His #status predicted

Query Match 67.0%; Score 59; DB 2; Length 214;

Best Local Similarity 60.0%; Pred. No. 0.38;

Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVIMGAPGSGKGT 17

DB 1 MRLILGAPGAGKGT 15

RESULT 15

C82255

adenylate kinase VC0986 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: C82255

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: C82255

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-214 <HE1>

A:Cross-references: GB:AE004180; GB:AE003852; NID:99655445; PIDN:AAF94147.1; GSPDB:GN.

A:Experimental source: serogroup O1, strain N16961, biotype El Tor

C:Genetics:

A:Gene: VC0986

A:Map position: 1

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

F:80-85/Region: nucleotide-binding motif B #status atypical

F:30-84/Active site: Ser, Asp #status predicted

Query Match 67.0%; Score 59; DB 2; Length 214;

Best Local Similarity 60.0%; Pred. No. 0.38;

Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVIMGAPGSGKGT 17

DB 1 MRLILGAPGAGKGT 15

Search completed: April 24, 2003, 10:20:18

Job time : 44 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 ; Search time 15 Seconds
(Without alignments)
35.308 Million cell updates/sec

Title: US-10-006-190-1_COPY_6_23
Perfect score: 88
Sequence: 1 RLRAVIMGAPSGSGKGTV 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/laa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/laa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	227	2 US-08-829-027-1	Sequence 1, Appl1
2	88	100.0	227	3 US-09-225-366-1	Sequence 1, Appl1
3	88	100.0	227	4 US-09-149-476-377	Sequence 377, Appl1
4	84	95.5	227	2 US-08-829-027-3	Sequence 3, Appl1
5	84	95.5	227	2 US-08-829-027-4	Sequence 4, Appl1
6	84	95.5	227	3 US-09-225-366-3	Sequence 3, Appl1
7	84	95.5	227	3 US-09-225-366-4	Sequence 4, Appl1
8	77	87.5	223	2 US-08-829-027-5	Sequence 5, Appl1
9	77	87.5	223	3 US-09-225-366-5	Sequence 5, Appl1
10	58	65.9	438	4 US-08-915-4988-37	Sequence 37, Appl1
11	52	59.1	222	4 US-08-134-001C-3289	Sequence 3289, Appl1
12	50	56.8	197	2 US-08-879-561-5	Sequence 5, Appl1
13	49	55.7	194	2 US-08-879-561-11	Sequence 11, Appl1
14	49	55.7	194	2 US-08-879-561-12	Sequence 12, Appl1
15	48	54.5	282	4 US-09-222-939-17	Sequence 17, Appl1
16	48	54.5	288	4 US-09-134-001C-4963	Sequence 4963, Appl1
17	46	52.3	1463	1 US-08-157-005-3	Sequence 3, Appl1
18	46	52.3	1463	4 US-08-747-863-3	Sequence 3, Appl1
19	46	52.3	1463	4 US-09-565-864-3	Sequence 3, Appl1
20	45	51.1	283	4 US-09-222-939-2	Sequence 2, Appl1
21	45	51.1	2517	2 US-08-801-263A-5	Sequence 5, Appl1
22	45	51.1	2517	3 US-09-102-248-5	Sequence 5, Appl1
23	43	48.9	539	2 US-08-759-581B-20	Sequence 20, Appl1
24	43	48.9	539	4 US-09-304-711-20	Sequence 20, Appl1
25	43	48.9	539	4 US-09-173-281-20	Sequence 20, Appl1
26	43	48.9	1065	3 US-08-630-172-9	Sequence 9, Appl1
27	43	48.9	1065	4 US-09-375-419-9	Sequence 9, Appl1

28	43	48.9	1170	2 US-08-789-078-2	Sequence 2, Appl1
29	43	48.9	1170	2 US-08-752-633-2	Sequence 2, Appl1
30	43	48.9	1170	2 US-08-476-062A-42	Sequence 42, Appl1
31	43	48.9	1170	5 PCT-US95-04886-2	Sequence 2, Appl1
32	43	48.9	1170	5 PCT-US96-01314-42	Sequence 42, Appl1
33	43	48.9	3457	2 US-08-416-603-4	Sequence 4, Appl1
34	42	47.7	297	2 US-09-006-535-4	Sequence 4, Appl1
35	42	47.7	298	2 US-09-006-535-3	Sequence 3, Appl1
36	42	47.7	388	2 US-08-759-581B-9	Sequence 9, Appl1
37	42	47.7	388	4 US-09-304-711-9	Sequence 9, Appl1
38	42	47.7	388	4 US-09-173-281-9	Sequence 9, Appl1
39	42	47.7	475	4 US-09-212-247C-4	Sequence 4, Appl1
40	42	47.7	694	2 US-08-895-522-4	Sequence 4, Appl1
41	42	47.7	694	3 US-09-195-391-4	Sequence 4, Appl1
42	42	47.7	1408	1 US-08-612-521-2	Sequence 2, Appl1
43	42	47.7	1408	1 US-09-134-001C-4471	Sequence 4471, Appl1
44	41	46.6	311	4 US-08-775-009-33	Sequence 33, Appl1
45	41	46.6	318	2 US-08-671-947-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-829-027-1
Sequence 1, Application US/08829027
Patent No. 5856160
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,027
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 2122022
US-08-829-027-1
Query Match 100.0%; Score 88; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

OY 1 RLRAVIMGAPSGSGKTIV 18
DB 6 RLRAVIMGAPSGSGKTIV 23

RESULT 2

US-09-225-366-1
Sequence 1, Application US/09225366
Patent No. 6001624
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purni
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLYATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,366
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,027
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 2122022
US-09-225-366-1
Query Match 100.0%; Score 88; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGSGKTIV 18
DB 6 RLRAVIMGAPSGSGKTIV 23

RESULT 3

US-09-149-476-377
Sequence 377, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
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EARLIER APPLICATION NUMBER: 60/057,650
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EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 100.0%; Score 88; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 1,1e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLRAVINGAPSGKGV 18
|||||
Db 6 RLRAVINGAPSGKGV 23

RESULT 4
US-08-829-027-3
Sequence 3, Application US/08829027
Patent No. 5856160
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

Db 6 RLRAVIMGAPGSGKT 23

RESULT 7

US-09-225-366-4
; Sequence 4, Application US/09225366
; Patent No. 6001624
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLYATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,366
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,027
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 450312
; US-09-225-366-4

Query Match 95.5%; Score 84; DB 3; Length 227;
Best local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLRAVIMGAPGSGKT 17
Db 6 RLRAVIMGAPGSGKT 22

RESULT 8
US-08-829-027-5
; Sequence 5, Application US/08829027
; Patent No. 5856160
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLYATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,027
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 28577
US-08-829-027-5

Query Match

Best local Similarity 87.5%; Score 77; DB 2; Length 223;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLRAVIMGAPGSGKT 18
Db 4 RLRAVIMGAPGSGKT 21

RESULT 9

US-09-225-366-5
; Sequence 5, Application US/09225366
; Patent No. 6001624
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLYATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,366
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,027
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 28577
US-09-225-366-5

Query Match 87.5%; Score 77; DB 3; Length 223;
Best Local Similarity 83.3%; Pred. No. 0.00044;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLRAVIMGAPSGSGKT 18
Db 4 KLRVAVILGPPGSGKGT 21

RESULT 10
US-08-915-4988-37
Sequence 37, Application US/089154988
Patent No. 6132954
GENERAL INFORMATION:
APPLICANT: James R. Lupski, Robert A. Britton, Donald L.
TITLE OF INVENTION: Methods of Screening for Agents that
TITLE OF INVENTION: Delay a Cell Cycle and Compositions Comprising ERA and an Anal
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESS: 8 No. 6132954Fis LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,4988
FILING DATE: August 20, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,353
FILING DATE: August 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 438
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-915-4988-37

Query Match 65.9%; Score 58; DB 4; Length 438;

Best Local Similarity 55.6%; Pred. No. 0.5;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLRAVIMGAPSGSGKT 18
Db 113 RLRAVILGAPNAGKSTL 130

RESULT 11
US-09-134-001C-3289
Sequence 3289, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: CTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3289
LENGTH: 222
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3289

Query Match 59.1%; Score 52; DB 4; Length 222;
Best Local Similarity 53.3%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 LRAVIMGAPSGSGKT 17
Db 8 MWITLMGLPGAGKT 22

RESULT 12
US-08-879-561-5
Sequence 5, Application US/08879561
Patent No. 5817482
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hallman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,561
FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0325 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CORPNOTO2
CLONE: 1484821
US-08-879-561-5

Query Match 56.8%; Score 50; DB 2; Length 197;
Best Local Similarity 81.8%; Pred. No. 3.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 IMGAPGSGKGT 17
Db 16 IIGGPGSGKGT 26

RESULT 13
US-08-879-561-11
Sequence 11, Application US/08879561
Patent No. 5817482
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
CLASSIFICATION: 424
FILING DATE: Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0325 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-879-561-11

Query Match 55.7%; Score 49; DB 2; Length 194;

Best Local Similarity 72.7%; Pred. No. 4.5;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 IMGAPGSGKGT 17
Db 13 VVGPGSGKGT 23

RESULT 14
US-08-879-561-12
Sequence 12, Application US/08879561
Patent No. 5817482
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
CLASSIFICATION: 424
FILING DATE: Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0325 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-879-561-12

Query Match 55.7%; Score 49; DB 2; Length 194;
Best Local Similarity 72.7%; Pred. No. 4.5;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 IMGAPGSGKGT 17
Db 14 VVGPGSGKGT 24

RESULT 15
US-09-222-939-17
Sequence 17, Application US/09222939
Patent No. 6372448
GENERAL INFORMATION:
APPLICANT: Filtz, Christian
APPLICANT: Youngman, Phillip
APPLICANT: Guzman, Luz-Marle
TITLE OF INVENTION: USE OF YLOF, YQEG, YVBO, YERL, AND YSXC, ESSENTIAL BACTERIAL

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 ; Search time 35 Seconds

(without alignments)
68.529 Million cell updates/sec

Title: US-10-006-190-1_COPY_6_23

Perfect score: 88

Sequence: 1 RLRAVIMGAPGSGKTV 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	227	19	AAW81101 Human mitochondria
2	88	100.0	227	19	AAW74787 Human secreted pro
3	88	100.0	227	21	AAW12440 Human mitochondria
4	88	100.0	227	22	AAW38899 Human polypeptide
5	88	100.0	227	22	AAW92887 Human protein sequ
6	88	100.0	227	22	AAW93066 Human protein sequ
7	88	100.0	227	22	AAW93487 Human protein sequ
8	88	100.0	227	22	AAW85885 Human adenylate ki
9	88	100.0	239	22	ABW12326 Human secreted pro
10	88	100.0	239	22	AAW40685 Human polypeptide

11	88	100.0	256	22	AAW3865 Human colon cancer
12	84	95.5	227	21	AAW12441 AK3 protein sequen
13	77	87.5	224	22	AAW11778 Human kinase (PKIN
14	74	84.1	216	22	AAW62530 Drosophila melanog
15	70	79.5	214	21	AAW53619 Human colon cancer
16	64	72.7	203	22	AAW42464 Propionibacterium
17	62	70.5	335	22	AAW23968 Novel human diago
18	61	69.3	245	20	AAW37077 Protein involved i
19	60	68.2	106	21	AAW01367 Human secreted pro
20	60	68.2	215	21	AAW36349 pseudomonas aerugi
21	60	68.2	232	20	AAW77257 Human adenylate ki
22	60	68.2	237	23	AAW41753 Human ovarian anti
23	60	68.2	238	22	AAW19263 Novel human diago
24	59	67.0	214	22	AAW34482 E. coli cellular p
25	59	67.0	214	22	AAW36040 Klebsiella pneumon
26	59	67.0	214	22	AAW38124 Salmonella typhi c
27	59	67.0	648	22	AAW26095 Novel human diago
28	58	65.9	86	22	AAW99570 ERA binding domain
29	58	65.9	158	21	AAW02190 Human secreted pro
30	58	65.9	342	21	AAW56160 Human secreted pro
31	58	65.9	437	20	AAW28519 Human regulatory p
32	58	65.9	437	22	AAW40298 Human polypeptide
33	58	65.9	437	22	AAW94547 Human protein sequ
34	58	65.9	438	22	AAW35620 Human ERA protein.
35	58	65.9	443	22	AAW42084 Human polypeptide
36	57	64.8	215	23	AAW48830 Listeria monocytog
37	57	64.8	237	22	AAW59655 Drosophila melanog
38	56	63.6	214	22	AAW35415 Haemophilus Influe
39	56	63.6	224	22	AAW36634 Staphylococcus aur
40	56	63.6	224	22	AAW37231 Staphylococcus aur
41	55	62.5	74	22	AAW43756 Peptide #11262 enc
42	55	62.5	74	22	AAW77489 Human bone marrow
43	55	62.5	74	22	AAW21416 Peptide #7850 enco
44	55	62.5	74	22	AAW37653 Peptide #11690 enc
45	55	62.5	74	23	AAW46511 Human peptide enco

ALIGNMENTS

AAW81101

RESULT 1
ID AAW81101 standard; Protein; 227 AA.

AC AAW81101;

DT 29-JAN-1999 (first entry)

DE Human mitochondrial adenylate kinase protein.

KW Human; mitochondrial; adenylate kinase; therapeutic;

KW neurological disorder; Alzheimer; Huntington; epilepsy; cancer;

KW neural; inflammation; immune.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 182 /note="Xaa is unspecified, encoded by NCA"

FT Misc-difference 185 /note="Xaa is unspecified, encoded by GNA"

FT W09844124-A1.

PD 08-OCT-1998.

PF 30-MAR-1998; 98WC-US06249.

PR 31-MAR-1997; 97US-0829027.

PA (INCY-) INCYTE PHARM INC.

XX HILLMAN JL, Shah P;

XX WPI: 1998-557119/47.
DR N-PSDB; AAV68223.
PT Human mitochondrial adenylate kinase, HMAK - useful e.g. to treat
PT neurological disorders such as Alzheimer's and screen for
XX antagonists for treatment of cancer or immunological disorders
PS Claim 5; Fig 1; 63pp; English.
XX
CC The human mitochondrial adenylate kinase (HMAK) protein of 227 amino
CC acids) can be administered therapeutically, especially by expressing
CC encoding polypeptides, to treat neurological disorders e.g. Alzheimer's
CC disease, Huntington's disease, epilepsy. It can be combined with a
CC suitable carrier in pharmaceutical compositions, which can be
CC administered to treat such disorders. HMAK was shown to have chemical
CC and structural homology with adenylate kinase isozyme 3 (AK3) from cow,
CC rat and human (92, 91 and 57 % identity respectively) and was expressed
CC in e.g. cancerous tissues, brain and neural tissues and tissues involved
CC in inflammation and the immune response. Increased activity or
CC expression was proposed to be associated with cancer and immunological
CC disorders, and decreased activity/expression with the development of
CC neurological disorders. Products of the above invention may be used in
CC the diagnosis and treatment of the above diseases and disorders.
XX
SQ Sequence 227 AA:

Query Match 100.0%; Score 88; DB 19; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGSKGV 18
| | | | | | | | | | | | | | | | | | | | | |
Db 6 RLRAVIMGAPSGSKGV 23

RESULT 2
AAW74787
ID AAW74787 standard: Protein; 227 AA.
XX

AC AAW74787;

XX 19-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 58 clone HHRHN61.

XX Human; secreted protein; testis; tumour; foetal brain tissue;

KW fusion protein; cancer; central nervous system; seizure;

KW diagnosis; neurodegenerative disease.

XX Homo sapiens.

OS Homo sapiens.

PN WO9839448-A2.

PD 11-SEP-1998.

PF 06-MAR-1998; 98MO-US04493.

XX 02-OCT-1997; 97US-0061060.

PR 07-MAR-1997; 97US-0038621.

PR 07-MAR-1997; 97US-0040161.

PR 07-MAR-1997; 97US-0040162.

PR 07-MAR-1997; 97US-0040163.

PR 07-MAR-1997; 97US-0040333.

PR 07-MAR-1997; 97US-0040334.

PR 07-MAR-1997; 97US-0040336.

PR 11-APR-1997; 97US-0043311.

PR 11-APR-1997; 97US-0043312.

PR 11-APR-1997; 97US-0043313.

PR 11-APR-1997; 97US-0043314.

PR 11-APR-1997; 97US-0043568.

PR 11-APR-1997; 97US-0043569.

PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047591.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.

PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0056915.
 PR 05-SEP-1997; 97US-0057669.
 PR 05-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
 PI Feng P, Ferlie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX
 DR WPI: 1998-506364/43.
 DR N-PSDB: AAV59568.
 XX
 PT New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 1: Page 575-576; 721pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the nucleic
 CC acid molecule designated Gene 58 from the human cDNA clone HHFHM61
 CC (deposited as clone ATCC 97899 and ATCC 209045).
 CC The gene can be used to generate fusion proteins by linking to the gene
 CC to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the
 CC stability of the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-V59812; amino acid sequences AAV74731-W5026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).
 CC
 XX
 SQ Sequence 227 AA;
 Query Match 100.0%; Score 88; DB 19; Length 227;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RLLRAVINGAPGSGKGTV 18
 DB 6 RLLRAVINGAPGSGKGTV 23
 RESULT 3
 AABI2440
 ID AABI2440 standard; Protein: 227 AA.
 XX
 AC AABI2440;
 XX
 DT 20-OCT-2000 (first entry)
 DE Human mitochondrial GTP:AMP phosphotransferase SEQ ID NO:4.
 KW Human: mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide.
 XX
 OS Homo sapiens.
 XX
 PN CN1249340-A.
 XX
 PI 05-APR-2000.
 XX

PF 28-SEP-1998; 98CN-0119439.
 XX
 PR 28-SEP-1998; 98CN-0119439.
 XX
 PA (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
 XX
 PI Yu L, Zhao Y, Bi A;
 XX
 DR WPI: 2000-400718/35.
 DR N-PSDB: AAA60582.
 XX
 PT Preparation of human mitochondrial matrix GTP : AMP phosphotransferase,
 PT its encode sequence -
 XX
 PS Claim 4: Page 14-15; 20pp; Chinese.
 XX
 CC The present invention describes a new ribotide sequence of human gene,
 CC that is, the cDNA sequence of human mitochondrial matrix GTP:AMP
 CC phosphotransferase (GTP3P) and the encoded polypeptide. The present
 CC sequence represents human GTP3P.
 CC
 XX
 SQ Sequence 227 AA;
 Query Match 100.0%; Score 88; DB 21; Length 227;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RLLRAVINGAPGSGKGTV 18
 DB 6 RLLRAVINGAPGSGKGTV 23
 RESULT 4
 AAM38899
 ID AAM38899 standard; Protein: 227 AA.
 XX
 AC AAM38899;
 XX
 DT 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 2044.
 KW Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.

DR	N-PSDB:AA158055.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
XX	
XX	
XX	Example 3; SEQ ID NO 2044; 10078bp; English.
CC	The invention relates to human nucleic acids (AA157798-AA161369) and
CC	the encoded polypeptides (AA038642-AA042213) with nootropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC	utiligation of the activities such as: immune system suppression,
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukemias and
CC	C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification.
XX	
SQ	Sequence 227 AA:
Query Match	100.0%; Score 88; DB 22; Length 227;
Best Local Similarity	100.0%; Pred. No. 0.0001;
Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RLLRAVIMGAPSGSGKTV 18
DB	6 RLLRAVIMGAPSGSGKTV 23
RESULT 5	
AAB92887	
ID	AAB92887 standard; Protein; 227 AA.
XX	
AC	AAB92887;
XX	
DT	26-JUN-2001 (first entry)
XX	
DE	Human protein sequence SEQ ID NO:11492..
XX	
XX	Human; primer: detection; diagnosis; antisense therapy; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	EP1074617-A2.
XX	
PD	07-FEB-2001.
XX	
XX	28-JUL-2000; 2000EP-0116126.
XX	
XX	29-JUL-1999; 99JP-0248036.
PR	27-AUG-1999; 99JP-0300253.
PR	11-JAN-2000; 2000JP-0118776.
PR	02-MAY-2000; 2000JP-0183767.
PR	09-JUN-2000; 2000JP-0241899.
XX	
PA	(HELI-) HELIX RES INST.
XX	
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI	Ishii S, Sugiyama T, Wakamatsu A, Negai K, Otsuki T;
XX	
DR	WPI; 2001-318749/34.
XX	
PT	Primer sets for synthesizing polynucleotides, particularly the 5602
PT	full-length cDNAs defined in the specification, and for the detection
PT	and/or diagnosis of the abnormality of the proteins encoded by the
PT	full-length cDNAs -
XX	

PS Claim 8; SEQ ID 11492; 2537pp + CD ROM; English.

xx The present invention describes primer sets for synthesizing 5602

CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and

CC in gene therapy. The primers are useful for synthesizing polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632

CC represent oligonucleotides, all of which are used in the exemplification

CC of the present invention.

CC XX

Sequence 227 AA:

Query Match 100.0%; Score 88; DB 22; length 227;

Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 18; conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 RLLRAVIMAGPSGSKCTV 18

|||||

DB 6 RLLRAVIMAGPSGSKCTV 23

```

RESULT 6
AAB93066
ID AAB93066 standard; Protein: 227 AA.
XX
AC AAB93066;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:11883.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI: 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -

```

XX Claim 8; SEQ ID 11883; 2537pp + CD ROM; English.

PS The present invention describes primer sets for synthesizing 5602

XX full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and

CC in gene therapy. The primers are useful for synthesizing polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632

CC represent oligonucleotides, all of which are used in the exemplification

CC of the present invention.

XX Sequence 227 AA:

Query Match 100.0%; Score 88; DB 22; Length 227;

Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGKGTV 18

Db 6 RLRAVIMGAPSGKGTV 23

RESULT 7

ID AAB93487 standard; Protein; 227 AA.

XX AAB93487;

DT 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:12786.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI: 2001-318749/34.

PT full-length cDNAs -

XX Claim 8; SEQ ID 12786; 2537pp + CD ROM; English.

PS The present invention describes primer sets for synthesizing 5602

XX full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and

CC in gene therapy. The primers are useful for synthesizing polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632

CC represent oligonucleotides, all of which are used in the exemplification

CC of the present invention.

XX Sequence 227 AA:

Query Match 100.0%; Score 88; DB 22; Length 227;

Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGKGTV 18

Db 6 RLRAVIMGAPSGKGTV 23

RESULT 8

ID AAB85885 standard; Protein; 227 AA.

XX AAB85885;

DT 30-NOV-2001 (first entry)

XX Human adenylate kinase 3 (AK3)-like protein.

XX Adenylate kinase 3-like protein; AK3-like protein; AK3; cell morphology;

XX MELAS; central nervous system disorder; epilepsy; skeletal muscle;

XX muscle disease; electron transfer disorder; Leber disease; human;

XX diabetes mellitus; Pearson disease; Parkinson's disease.

XX Homo sapiens.

XX WO200109346-A1.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-JP05066.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 18-OCT-1999; 99US-0159590.

XX 11-JAN-2000; 2000JP-0118776.

XX 17-FEB-2000; 2000US-0183322.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Hayashi K, Saito K, Yamamoto J, Ishii S;

XX Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Ihara S, Nakae H;

XX Nishikawa T, Kimura K;

DR WPI: 2001-564737/63.
 DR N-PSDB: AAA47197.
 XX
 PT New gene encoding an adenylate kinase 3-like protein, and the protein
 PT and antibodies to it, useful for diagnosis of brain disease e.g.
 PT epilepsy, muscle disease, genetic disorder, diabetes
 PS
 PS Claim 1; Page 34-35; 41pp; Japanese.
 XX
 CC The invention relates to a cDNA (clone C-WT28P2000329) encoding a novel
 CC adenylate kinase 3 (AK3)-like protein. C-WT28P2000329 has functions of
 CC converting extracellular signals into intracellular signals and changing
 CC cell morphology. The AK3-like protein, polynucleotides and antibodies are
 CC useful in the investigation of diseases such as MEAS (cerebral accident
 CC condition with hyperlactacidemia), central nervous system disorder,
 CC epilepsy, skeletal muscle conditions, muscle disease, electron transfer
 CC disorders, liver disease, diabetes mellitus, Pearson disease, Parkinson's
 CC disease, metabolism disorders. They are useful for developing diagnostics
 CC and treatment agents. The present sequence represents the human AK3-like
 CC protein of the invention.
 CC
 SO Sequence 227 AA:
 Query Match 100.0%; Score 88; DB 22; Length 227;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY I RLRAVIMGAPSGSGKTV 18
 Db 6 RLRAVIMGAPSGSGKTV 23
 ID ABB12326 standard; peptide: 239 AA.
 AC ABB12326;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human secreted protein homologue, SEQ ID NO:2696.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
 KW antifungal; antiviral; antitumor.
 XX
 OS Homo sapiens.
 PN NO200157188-A2.
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001MO-US03800.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-457740/49.
 DR N-PSDB: ABA09570.

XX
 PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX
 PS Claim 20; Page 333; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.
 CC
 SO Sequence 239 AA:
 Query Match 100.0%; Score 88; DB 22; Length 239;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY I RLRAVIMGAPSGSGKTV 18
 Db 18 RLRAVIMGAPSGSGKTV 35
 ID AAM40685 standard; protein: 239 AA.
 AC AAM40685;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 5616.
 XX
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX

```

OS Homo sapiens.
XX
XX EN WO20015312-A1.
XX
XX PD 26-JUL-2001.
XX
XX PF 26-DEC-2000; 2000WO-US34263.
XX
XX PR 21-JAN-2000; 2000US-0488725.
XX
XX PR 25-APR-2000; 2000US-0552317.
XX
XX PR 09-JUL-2000; 2000US-0598042.
XX
XX PR 19-JUL-2000; 2000US-0620312.
XX
XX PR 03-AUG-2000; 2000US-0653450.
XX
XX PR 14-SEP-2000; 2000US-0662191.
XX
XX PR 19-OCT-2000; 2000US-0693036.
XX
XX PR 29-NOV-2000; 2000US-0727344.
XX
XX PA (HYSEQ-) HYSEQ INC.
XX
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX DR WPI: 2001-442253/47.
XX
XX DR N-PSDB: AAI59841.
XX
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries -
XX
XX PS Example 2; SEQ ID NO 5616; 10078pp; English.
XX
XX CC The invention relates to human nucleic acids (AA157798-AA161369) and
XX CC the encoded polypeptides (AAW38642-AAW42213) with nootropic,
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification.
XX
XX SO Sequence 239 AA:
XX
XX Query Match 100.0%; Score 88; DB 22; Length 239;
XX Best Local Similarity 100.0%; Pred. No. 0.00011;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX Y 1 RLLRAVINGAPSGSGKTV 18
XX ||||||||||||||||
XX Db . 18 RLLRAVINGAPSGSGKTV 35
XX
XX RESULT 11
XX AAG73865
XX ID AAG73865 standard; Protein; 256 AA.
XX
XX AAG73865;
XX
XX DT 03-SEP-2001 (first entry)
XX
XX DE Human colon cancer antigen protein SEQ ID NO:4629.
XX
XX KW Human: colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma.
XX
XX OS Homo sapiens.

```

PN	XX	W0200122920-A2.
XX	XX	
PD	XX	05-APR-2001.
XX	XX	
PF	XX	28-SEP-2000; 2000WO-US26524.
XX	XX	
PR	XX	29-SEP-1999; 99US-0157137.
PR	XX	03-NOV-1999; 99US-0163280.
XX	XX	
PA	XX	(HUMA-) HUMAN GENOME SCI INC.
PI	XX	
PI	XX	Ruben SM, Barash SC, Birse CE, Rosen CA;
DR	XX	WPI; 2001-235357/24.
DR	XX	N-PSDB; AAH33296.
PT	XX	
PT	XX	Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX	XX	useful for preventing, diagnosing and/or treating colorectal cancers -
XX	XX	
XX	XX	Claim 11; Page 6430-6431; 9803pp; English.
XX	XX	
CC	CC	AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC	CC	cancer-associated nucleic acid molecules (N) and proteins (P), where
CC	CC	the proteins are collectively known as colon cancer antigens. The colon
CC	CC	cancer antigens have cytostatic activity and can be used in gene
CC	CC	therapy and vaccine production. N and P may be used in the prevention,
CC	CC	diagnosis and treatment of diseases associated with inappropriate P
CC	CC	expression. For example, N and P may be used to treat disorders
CC	CC	associated with decreased expression by rectifying mutations or deletions
CC	CC	in a patient's genome that affect the activity of P by expressing
CC	CC	inactive proteins or to supplement the patients own production of P.
CC	CC	Additionally, N may be used to produce the colon cancer-associated Ps,
CC	CC	by inserting the nucleic acids into a host cell and culturing the cell
CC	CC	to express the proteins. N and P can be used in the prevention, diagnosis
CC	CC	and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC	CC	and AAB77789 represent sequences used in the exemplification of the
CC	CC	present invention.
CC	CC	N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC	CC	missing at time of publication, meaning no sequences are present for
CC	CC	SEQ ID NO:1027 to 1052, 7921 and 7922.
SO	XX	
XX	XX	Sequence 256 AA;
XX	XX	
Query Match		100.0%; Score 88; DB 22; Length 256;
Best Local Similarity		100.0%; Pred. No. 0.00011;
Matches 18; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	1	RLRAVINGAPGSGKGTV 18
DB	35	RLRAVINGAPGSGKGTV 52
RESULT 12		
AAB12441		
ID	AAB12441	standard; Protein; 227 AA.
XX	XX	
AC	AC	AAB12441;
XX	XX	
XX	XX	20-OCT-2000 (first entry)
DE	DE	
XX	XX	AK3 protein sequence.
XX	XX	
KW	KW	Human; mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide.
OS	OS	Unidentified.
PN	PN	
PN	PN	CN1249340-A.
XX	XX	
PD	PD	05-APR-2000.
XX	XX	
PF	PF	28-SEP-1998; 98CN-0119439.
XX	XX	

PR		28-SEP-1998;	98CN-0119439.
XX			
PA	(XINH-)	XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.	
XX			
PI	Yu L,	Zhao Y,	Bi A;
XX			
DR	WPI:	2000-400718/35.	
N-P	PSTDB:	AAA60585.	
XX			
PT	Preparation of human mitochondrial matrix GTP :	AMP phosphotransferase,	
PT	its encode sequence -		
XX			
PS	Example 2; Fig 2:	20pp; Chinese.	
XX			
CC	The present invention describes a new ribotide sequence of human gene,		
CC	that is, the cDNA sequence of human mitochondrial matrix GTP:AMP		
CC	phosphotransferase (GTP:P) and the encoded polypeptide. The present		
CC	sequence represents the AK3 protein sequence which is used in		
CC	comparison with human GTP:P in the present invention.		
XX			
SQ	Sequence	227 AA;	
Query Match	95.5%;	Score 84;	DB 21; Length 227;
Best Local Similarity	94.4%;	Pred. No. 0.00037;	
Matches	17; Conservative	0;	Mismatches 1; Indels 0; Gaps 0.
OY	1 RLLRAVINGAPSGKGTV 18		
Dd	6 RLLRAAIMGAPSGKGTV 23		
RESULT 13			
AEE11778			
ID	AEE11778 standard; Protein;	224 AA.	
XX			
AC	AEE11778;		
XX			
DT	18-DEC-2001 (first entry)		
XX			
DE	Human kinase (PKIN)-12 protein.		
KW	Human kinase (PKIN); gene therapy; adenocarcinoma; immune disorder; gout;		
KW	Cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome;		
KW	AIDS; Addison's disease; microbial infection; inflammation; osteoporosis;		
KW	atherosclerosis; cardiovascular disease; myocardial infarction; anaemia;		
KW	mysthenia gravis; cirrhosis; catarract; growth and development disorder;		
KW	seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder;		
KW	lipid storage disease; Pick's disease; Tay-Sachs disease; renal disease;		
KW	obesity; restorative therapy; immunomodulatory vaccine; cardiovascular;		
KW	antimicrobial; cytostatic; antiinflammatory; asthma.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Region	1..126	/note= "Adenylate kinase"
FT	Region	8..23	/note= "Shikimate kinase family"
FT	Region	9..25	/note= "Adenylate kinase"
FT	Region	10..190	/note= "Adenylate kinase"
FT	Region	33..76	/note= "Adenylate kinase"
FT	Region	80..94	/note= "Adenylate kinase"
FT	Domain	85..96	/note= "Adenylate kinase motif"
FT	Region	107..124	/note= "Shikimate kinase family"
FT	Region	132..162	/note= "Adenylate kinase"
FT			
XX			

```

PN WO200181555-A2.
XX
XX 01-NOV-2001.
PF
XX 20-APR-2001; 2001WO-US12992.
XX
PR 20-APR-2000; 2000US-199021P.
PR 28-APR-2000; 2000US-200226P.
PR 05-MAY-2000; 2000US-202339P.
PR 11-MAY-2000; 2000US-203505P.
PR 18-MAY-2000; 2000US-205564P.
PR 26-MAY-2000; 2000US-207739P.
PR 01-JUN-2000; 2000US-208795P.
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB;
PI Bandman O, Lu DMW, Lal P, Burford N, Khan FA, Walla NK, Yao MG;
PI Patterson C, Burrill JD, Marcus GA, Zingler KA, Reclison SA, Lu Y;
PI Policky JL, Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MR;
PI Walsh RT, Ramkumar J, Borowsky ML, Au-young J, Hillman JL,
PI Gururajan R;
DR WPI: 2001-611740/70.
DR N-PESDB: AAD18827.
PT Human kinases and nucleic acids, useful for preventing diagnosing and
PS treating cancers, inflammation and immune disorders -
XX
XX Claim 1; Page 138-139; 16pp; English.
CC The present invention relates to human kinases (PKIN) and the nucleic
CC acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is
CC used in the prevention, diagnosis and treatment of diseases cancers,
CC adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease,
CC acquired immune deficiency syndrome (AIDS), anaemia, asthma, allergies,
CC gout, microbial infections, cardiovascular disease and/or inflammation,
CC myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial
CC interaction, cataract, growth and development disorder, seizure disorder,
CC pulmonary embolism, Gaucher's disease, lipid disorder, lipid storage
CC disease, Pick's disease, Tay-Sachs disease, renal disease and obesity.
CC PKIN may be used to treat disorders associated with decreased PKIN
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of PKIN by expressing inactive proteins or to
CC supplement the patient's own production of PKIN. PKIN nucleic acids may be
CC used to produce the PKIN polypeptide, by inserting the nucleic acids into
CC a host cell and culturing the cell to express the protein. PKIN nucleic
CC acid and its complementary sequences may also be used as DNA probes in
CC diagnostic assays to detect and quantitate the presence of similar
CC nucleic acid sequences in samples and therefore which patients may be
CC in need of restorative therapy. The present sequence is human PKIN-12
CC protein.
XX
XX Sequence 224 AA:
SQ
OY 1 RLRAVINGAPSGKGTGTV 18
ID :|||||:|||||||
AB B62530
ID ABB62530 standard; Protein: 216 AA.
XX
XX ABB62530;
DT 26-MAR-2002 (first entry)
DE Drosophila melanogaster polypeptide SEQ ID NO 14382.

```

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, LI PWD, Myers EM;
 XX
 DR MPI; 2001-656860/75.
 DR N-PSDB; ABL06633.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Disclosure; SEQ ID NO 14382; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABLI6176-ABJ30511), expressed DNA
 CC sequences (ABLI6176-ABLI6175) and the encoded proteins
 CC (ABBS7737-ABBS72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 216 AA;
 Query Match 84.1%; Score 74; DB 22; Length 216;
 Best Local Similarity 72.2%; Pred. No. 0.0088;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RLRAVIMGAPGSGKTV 18
 : : ||||:|||||||:
 Db 4 KIFRAVIGAPGSGKGTI 21
 : : ||||:|||||||:
 RESULT 15
 AAB53619 ID AAB53619 standard; Protein; 214 AA.
 XX
 AC AAB53619;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Human colon cancer antigen protein sequence SEQ ID NO:1159.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200055351-A1.
 XX

PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05883.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR MPI; 2000-587534/55.
 DR N-PSDB; AAC98376.
 XX
 PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -
 XX
 XX Claim 11: Page 1741-1742; 2104pp; English.
 XX
 PS AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 214 AA;
 Query Match 79.5%; Score 70; DB 21; Length 214;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 AVIMGAPGSGKTV 18
 |||||:|||||||:
 Db 1 AVIMGAPGSGKTV 14
 : : |||||:|||||||:
 Search completed: April 24, 2003, 10:19:29
 Job time : 37 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 ; Search time 29 Seconds
(without alignments)
127.891 Million cell updates/sec

Title: US-10-006-190-1_COPY_6_23
Perfect score: 88
Sequence: 1 RLRAVINGAPSGKGV 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTRMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	189	11 Q9D8W6	Q9D8W6 mus musculus
2	88	100.0	227	4 Q9NP84	Q9NP84 h cDNA flj1
3	88	100.0	227	6 Q95J94	Q95J94 oryctolagus
4	88	100.0	227	11 Q9D8W5	Q9D8W5 mus musculus
5	88	100.0	227	11 Q9D8W5	Q9D8W5 mus musculus
6	88	100.0	227	11 Q9D721	Q9D721 mus musculus
7	88	100.0	227	11 Q9D721	Q9D721 mus musculus
8	74	84.1	216	5 Q9VG06	Q9VG06 dirosophila
9	65	73.9	231	3 Q93985	Q93985 neocallimias
10	65	73.9	231	3 Q93987	Q93987 pironomys s
11	64	73.7	232	3 Q93986	Q93986 neocallimias
12	62	70.5	55	2 Q9XD16	Q9XD16 bacteroides
13	60	68.2	202	4 Q9KWA2	Q9KWA2 agrobacteri
14	60	68.2	232	11 Q9CY37	Q9CY37 homo sapien
15	58	65.9	130	11 Q9RA46	Q9RA46 mus musculus
16	58	65.9	248	11 Q9ESCA	Q9ESCA mus musculus

17	58	65.9	331	11 Q9ESCA	Q9ESCA mus musculus
18	58	65.9	437	4 Q96RC0	Q96RC0 homo sapien
19	58	65.9	437	4 Q9WY4	Q9WY4 homo sapien
20	58	65.9	437	11 Q9CZ04	Q9CZ04 mus musculus
21	58	65.9	437	11 Q9CZ04	Q9CZ04 mus musculus
22	58	65.9	444	4 Q96LE2	Q96LE2 homo sapien
23	57	64.8	237	5 Q9W1D0	Q9W1D0 dirosophila
24	57	64.8	240	5 Q9U915	Q9U915 dirosophila
25	56	63.6	221	16 Q9R7X4	Q9R7X4 thermococcus
26	55	62.5	211	16 Q9RE31	Q9RE31 fusobacteri
27	55	62.5	220	5 Q9Y0A8	Q9Y0A8 cryptospori
28	55	62.5	229	5 Q964H2	Q964H2 plasmodium
29	54	61.4	222	5 Q9R5S3	Q9R5S3 trypanosoma
30	53	60.2	177	16 Q97G88	Q97G88 clostridium
31	53	60.2	248	10 Q9FK35	Q9FK35 arabidopsis
32	53	60.2	588	10 Q9VY11	Q9VY11 arabidopsis
33	52	59.1	191	5 Q20230	Q20230 caenorhabd
34	52	59.1	191	5 Q20230	Q20230 caenorhabd
35	52	59.1	193	11 Q920P5	Q920P5 mus musculus
36	52	59.1	196	16 Q9UE38	Q9UE38 agrobacteri
37	52	59.1	216	1 Q9P9D2	Q9P9D2 uncultured
38	52	59.1	262	16 Q9WZM6	Q9WZM6 thermotoga
39	52	59.1	283	10 Q9F1J7	Q9F1J7 arabidopsis
40	51	58.0	208	5 Q00846	Q00846 parametium
41	51	58.0	211	5 Q9U1D3	Q9U1D3 leishmania
42	51	58.0	510	12 Q65723	Q65723 barley str1
43	51	58.0	512	12 Q65718	Q65718 barley str1
44	51	58.0	512	12 Q65722	Q65722 barley str1
45	51	58.0	512	12 Q65725	Q65725 barley str1

ALIGNMENTS

RESULT 1

Q9D8W6

PRELIMINARY: PRT; 189 AA.

Q9D8W6: 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE 10 day old male pancreas cDNA, RIKEN full-length enriched library,
 clone:1810027K10, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavet T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochi H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barish G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.D., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 Functional annotation of a full-length mouse cDNA collection.;
 RT Nature 409:685-690(2001).
 CC -!- SIMILARITY: BELONGS TO THE ADENYLYATE KINASE FAMILY.
 DR EMBL: AK007618; BAB25139.1; -.

DR HSSP; P08760; 2AK3.
 DR InterPro: IPR000850; Adenylate_kin.
 DR EMBL: AK027534; BAB55183.1; -
 DR EMBL: BC013771; AAH13771.1; -
 DR HSSP; P08760; 2AK3.
 DR InterPro: IPR000850; Adenylate_kin.
 DR InterPro: IPR000623; Shik_kinase.
 DR Pfam: PF00406; adenylatekinase; 1.
 DR PRINTS; PR01004; ADENYLTKINASE.
 DR PRINTS; PR01100; SHIKMTKINASE.
 DR PRODOM; PD000657; adenylatekinase; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 KW Kinase; transferase.
 SQ SEQUENCE 189 AA; 21193 MW; 822ADB21804F5336 CRC64;

Query Match 100.0%; Score 88; DB 11; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAGSGKGV 18
 |||||
 DB 6 RLRAVIMGAGSGKGV 23

RESULT 2

ID Q9NPB4 PRELIMINARY; PRT; 227 AA.

AC Q9NPB4; 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE CNA FLJ11089 f1s, clone PLACE105305, highly similar to GTP:AMP

DE phosphotransferase mitochondrial (EC 2.7.4.10) (CDNA FLJ10691 f1s,

DE clone NT2RP200359, highly similar to GTP:AMP phosphotransferase

DE mitochondrial) (CDNA FLJ14628 f1s, clone NT2RP200329, highly similar

DE to GTP:AMP phosphotransferase mitochondrial) (Hypothetical 25.6 kDa

DE protein).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-PLACENTA;

RA Isegal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,

RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,

RA Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;

RT "NEDO human cDNA sequencing project."

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Isegal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,

RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,

RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,

RA Masuho Y., Kanehori K.;

RT "NEDO human cDNA sequencing project."

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Isegal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Shiraori A., Sudo H.,

RA Magatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Niomiya K., Iwayanagi T.;

RT "NEDO human cDNA sequencing project."

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE-LYMPH;

RA Strausberg R.;

CC Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

-1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

EMBL: AK001951; BAA91996.1; -

DR EMBL: AK001553; BAA91753.1; -
 DR EMBL: AK027534; BAB55183.1; -
 DR EMBL: BC013771; AAH13771.1; -
 DR HSSP; P08760; 2AK3.
 DR InterPro: IPR000850; Adenylate_kin.
 DR InterPro: IPR000623; Shik_kinase.
 DR Pfam: PF00406; adenylatekinase; 1.
 DR PRINTS; PR00094; ADENYLTKINASE.
 DR PRINTS; PR01100; SHIKMTKINASE.
 DR PRODOM; PD000657; adenylatekinase; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 KW Hypothetical protein; Kinase; transferase.
 SQ SEQUENCE 227 AA; 25565 MW; 98A0EDFAFD9C9CEF CRC64;

Query Match 100.0%; Score 88; DB 6; Length 227;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAGSGKGV 18
 |||||
 DB 6 RLRAVIMGAGSGKGV 23

RESULT 3

ID Q95J94 PRELIMINARY; PRT; 227 AA.

AC Q95J94; 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE Adenylate kinase 3.

DE Oryctolagus cuniculus (Rabbit).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-RENAL PROXIMAL TUBULE;

RX MEDLINE-21240235; PubMed-11342145;

RA Brochiero E., Condy M.J., Klein H., Laprade R., Lapointe J.Y.;

RT "Activation of an ATP-dependent K(+) conductance in Xenopus oocytes by

RT expression of adenylate kinase cloned from renal proximal tubules."

RL Biochem. Biophys. Acta 1510:29-42(2001).

CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

DR EMBL: AF417508; AAL07503.1; -

DR InterPro: IPR000850; Adenylate_kin.

DR Pfam: PF00406; adenylatekinase; 1.

DR PRODOM; PD000657; Adenylate_kin; 1.

DR PROSITE; PS00113; ADENYLATE_KINASE; UNKNOWN_1.

KW Kinase; transferase.

SQ SEQUENCE 227 AA; 25610 MW; ECDIDDF89228A4E CRC64;

Query Match 100.0%; Score 88; DB 6; Length 227;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAGSGKGV 18
 |||||
 DB 6 RLRAVIMGAGSGKGV 23

RESULT 4

ID Q9DBM5 PRELIMINARY; PRT; 227 AA.

AC Q9DBM5; 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE Adenylate kinase 3 alpha like.

GN AKL3L.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Noridone P., Ring B., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK004864; BAB23825.1; -.
DR HSSP: P08760; 2AK3.
DR MGD: MGI:1860835; AK131.
DR InterPro: IPR000850; Adenylate_kin.
DR InterPro: IPR000623; Shik_kinase.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PRO0094; ADENYLTKINASE.
DR PRINTS: PRO1100; SHIKMTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW kinase; Transferase.
SQ SEQUENCE 227 AA; 25427 MW; 660FDF1E991DE5AC CRC64;

Query Match 100.0%; Score 88; DB 11; Length 227;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVINGAPSGKGTV 18
DB 6 RLRAVINGAPSGKGTV 23
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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK005194; BAB23876.1; -.
DR HSSP: P08760; 2AK3.
DR MGD: MGI:1860835; AK131.
DR InterPro: IPR000850; Adenylate_kin.
DR InterPro: IPR000623; Shik_kinase.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PRO0094; ADENYLTKINASE.
DR PRINTS: PRO1100; SHIKMTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW kinase; Transferase.
SQ SEQUENCE 227 AA; 25427 MW; 660B7FBA971DE5AC CRC64;

Query Match 100.0%; Score 88; DB 11; Length 227;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVINGAPSGKGTV 18
DB 6 RLRAVINGAPSGKGTV 23
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RESULT 6
O9D721 PRELIMINARY: PRT: 227 AA.
AC O9D721;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Adenylate kinase 3 alpha like.
GN AK131.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamlya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

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RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK008681; BAB25829.1; -
DR EMBL: BC016432; AAH16432.1; -
DR EMBL: BC019174; AAH19174.1; -
DR EMBL: BC024871; AAH24871.1; -
DR HSSP: P08760; 2AK3.
DR MGD: MG11860835; AK131.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PRO0094; ADENYLTKINASE.
DR PRINTS: PRO1100; SHIKMTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
DR Kinase: Transferase.
SQ SEQUENCE 227 AA; 25426 MW; 6601DF10971DE5AC CRC64;

Query Match 100.0%; Score 88; DB 11; Length 227;
Best Local Similarity 100.0%; Pred. No. 7; Se-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLRAVIMGAPGSGKTV 18
Db 6 RLRAVIMGAPGSGKTV 23

RESULT 7
Q9VGU6 PRELIMINARY; PRT; 216 AA.
AC Q9VGU6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CG6612 protein (Adenylate kinase isozyme 3).
GN ADK3 OR DAK3 OR CG6612.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phrygotea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylvestre R., Teclor C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]

RP SEQUENCE FROM N.A.
RA Noma T.;
RT "DAK3.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AE003689; AAF54578.1; -
DR EMBL: AB050622; BAB4152.1; -
DR HSSP: P08760; 2AK3.
DR FlyBase: FBgn0042094; Adk3.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PRO0094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
DR Kinase: Transferase.
SQ SEQUENCE 216 AA; 24145 MW; 6AB49A756D23091B CRC64;

Query Match 84.1%; Score 74; DB 5; Length 216;
Best Local Similarity 72.2%; Pred. No. 0 0068;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLRAVIMGAPGSGKTV 18
Db 4 KIFRAVIMGAPGSGKTV 21

RESULT 8
Q93985 PRELIMINARY; PRT; 231 AA.
AC Q93985;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (Fragment).
GN HDGAKL2.1.
OS Neocallimastix frontalis (Rumen fungus).
OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
OC Neocallimastixaceae; Neocallimastix.
OX NCBI_TaxID=4757;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=12;
RA Voncken F., Boyma B., Verhagen E., van Wesel R., van der Drift C.,
RA Veenhuis M., Hackstein J., Vogels G.;
RT "Evidence for a chimeric origin of chytrid hydromycetes.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: A3224658; CAA12055.1; -
DR HSSP: P07170; 1AKY.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.

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DR PRINTS: PR00094: ADENYLTKINASE.
DR PRODOM: PD000657: Adenylate_kin. 1.
DR PROSITE: PS00113: ADENYLATE_KINASE; 1.
KW Kinase; transferase.
FT NON_TER 231 231
SQ SEQUENCE 231 AA; 25353 MW; 844B51EB554676A2 CRC64;

Query Match
Best Local Similarity 73.9%; Score 65; DB 3; Length 231;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LRAVINGAPSGSGKT 17
Db 10 LRMVIMGPSPSGKT 24

RESULT 9
OY 093987 PRELIMINARY; PRT; 231 AA.
AC 093987;
DT 01-MAY-1999 (TrEMBLrel. 10, Created).
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Adenylate kinase (EC 2.7.4.3) (Fragment).
GN HDGAK2.2.
OS Pteromyces sp. E2.
OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;
OC Neocallimastixaceae; Pteromyces.
ON NCBI_TaxID=73868;
RX [1]
RP SEQUENCE FROM N.A.
RA Voncken F., Boxma B., Verhagen E., van Wesel R., van der Drift C.,
RA Veenhuis M., Hackstein J., Vogels G.;
RT Evidence for a chimeric origin of chytrid hydrogcnosomes."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AJ224660; CA12057.1; -.
DR HSSP: P07170; 1AKY.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRODOM: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Kinase; transferase.
FT NON_TER 231 231
SQ SEQUENCE 231 AA; 25407 MW; 64279A95550570BF CRC64;

Query Match
Best Local Similarity 73.9%; Score 65; DB 3; Length 231;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LRAVINGAPSGSGKT 17
Db 10 LRMVIMGPSPSGKT 24

RESULT 10
OY 093986 PRELIMINARY; PRT; 232 AA.
AC 093986;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Adenylate kinase (EC 2.7.4.3) (Fragment).
GN HDGAK2.2.
OS Neocallimastix frontalis (Rumen fungus).
OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;
OC Neocallimastixaceae; Neocallimastix.
ON NCBI_TaxID=4757;
RX [1]
RP SEQUENCE FROM N.A.
RA Voncken F., Boxma B., Verhagen E., van Wesel R., van der Drift C.,

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RA Veenhuis M., Hackstein J., Vogels G.;
RT "Evidence for a chimeric origin of chytrid hydrogcnosomes."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AJ224659; CA12056.1; -.
DR HSSP: P07170; 1AKY.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRODOM: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Kinase; transferase.
FT NON_TER 232 232
SQ SEQUENCE 232 AA; 25441 MW; 1B74EFD7C97891F2 CRC64;

Query Match
Best Local Similarity 72.7%; Score 64; DB 3; Length 232;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 LRAVINGAPSGSGKT 17
Db 10 LRMVIMGPSPSGKT 24

RESULT 11
OY 09XD16 PRELIMINARY; PRT; 55 AA.
AC 09XD16;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)
DE (Fragment).
GN ADK.
OS Bacteroides fragilis.
OC Bacteria; CFP group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
OC Bacteroides.
ON NCBI_TaxID=817;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN-NCTC 9343;
RX MEDLINE-99307214; Pubmed-10377135;
RA Comstock L.E., Coyne M.J., Tzianabos A.O., Pantosti A.,
RA Onderdonk A.B., Kasper D.U.;
RT "Analysis of a capsular polysaccharide biosynthesis locus of
RT Bacteroides fragilis."
RL Infect. Immun. 67:3525-3532(1999).
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
DR EMBL: AF048749; AAD40729.1; -.
DR HSSP: P27142; 12IN.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRODOM: PD000657; Adenylate_kin; 1.
KW ATP-binding; Kinase; transferase.
FT NON_TER 55 55
SQ SEQUENCE 55 AA; 5849 MW; 027DCA433E12908A CRC64;

Query Match
Best Local Similarity 70.5%; Score 62; DB 2; Length 55;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 LRAVINGAPSGSGKT 17
Db 1 LRMVIMGPSPSGKT 16

RESULT 12

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09KMA2
ID 09KMA2 PRELIMINARY: PRT: 194 AA.
AC 09KMA2:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK OR R10RF82.
OS Agrobacterium rhizogenes.
OC Plasmid pRI1724.
OC Bacteria: Proteobacteria: alpha subdivision: Rhizobiaceae group;
OC Rhizobiaceae: Rhizobium.
OX NCBI_TaxID=339;
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN-MAFF03-01724; PLASMID-PR11724;
RA Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.;
RT "Analysis of unique variable region of a plant root inducing plasmid,
RL pRI1724, by the construction of its physical map and library.";
RN (2)
RN SEQUENCE FROM N.A.
RC STRAIN-MAFF03-01724; PLASMID-PR11724;
RA Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.;
RT "Genome structure of RI plasmid (1): Construction of linking library
RL and physical map of pRI1724 in Japanese Agrobacterium.";
RN (3)
RN SEQUENCE FROM N.A.
RC STRAIN-MAFF03-01724; PLASMID-PR11724;
RA Moriguchi K., Maeda Y., Satou M., Satuti N., Kataoka M., Tanaka N.,
RN Yoshida K.;
RT "The complete nucleotide sequence of a RI (root inducing) plasmid
RL indicates its chimerical structure between TI and Sym plasmids.";
RN (4)
RN Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RN (5)
RN SEQUENCE FROM N.A.
RC STRAIN-MAFF03-01724; PLASMID-PR11724;
RA Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.;
RT "Analysis of unique variable region of a plant root inducing plasmid,
RL pRI1724, by the construction of its physical map and library.";
RN (6)
RN Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RN (7)
RN SEQUENCE FROM N.A.
RC STRAIN-MAFF03-01724; PLASMID-PR11724;
RA MEDLINE-20241294; PubMed-10780382;
RA Maeda Y., Moriguchi K., Kataoka M., Satou M., Satuti N., Tanaka N.,
RN Yoshida K.;
RT "Genome structure of RI plasmid (1): Sequencing analysis of T-DNA and
RL its flanking regions of pRI1724 in Japanese Agrobacterium
RN rhizogenes.";
RN (8)
RN Nucleic Acids Symp. Ser. 42:67-68(1999).
RN (9)
RN FUNCTION: THIS SMALL UNBIOTICUS ENZYME IS ESSENTIAL FOR
RN MAINTENANCE AND CELL GROWTH (BY SIMILARITY).
RN (10)
RN CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
RN (11)
RN SUBUNIT: MONOMER (BY SIMILARITY).
RN (12)
RN SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
RN (13)
RN SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
RN EMBL: AB039932; BAA97793.1; -;
RN EMBL: AP002086; BAB16201.1; -;
RN HSP: P07170; LAKY.
RN InterPro: IPR000850; Adenylate_kin.
RN Pfam: PF00406; adenylatekinase.1.
RN PRINTS: PR00094; ADENYLTKINASE.
RN ProDom: PD000657; Adenylate_kin.1.
RN PROSITE: PS00113; ADENYLATE_KINASE.1.
RN ATP-binding: kinase, plasmid, transferase.
KW SEQUENCE 194 AA; 20468 MW; 533450AEF08F4F59 CRC64;

Query Match 68.2%; Score 60; DB 2; Length 194;
Best Local Similarity 66.7%; Pred. No. 0.58;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 LRAVINGAPGSGKGT 17
Db 1 MRLIMPGPGSGKGT 15
RESULT 13
O8TCY3
ID O8TCY3 PRELIMINARY: PRT: 202 AA.
AC O8TCY3:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adenylate kinase 2 variant AK2C.
GN AK2.
OS Homo sapiens (Human).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.
OX NCBI_TaxID=9606;
RN (1)
RN SEQUENCE FROM N.A.
RA Guo J.;
RT "Novel isoforms of Human Adenylate Kinase 2";
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY080899; AAL87027.1; -;
KW Kinase.
SQ SEQUENCE 202 AA; 22265 MW; AE7593A8ADBD00CF CRC64;

Query Match 68.2%; Score 60; DB 4; Length 202;
Best Local Similarity 66.7%; Pred. No. 0.6;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 LRAVINGAPGSGKGT 17
Db 16 IRAVLGPGPGGKGT 30
RESULT 14
O9CY37
ID O9CY37 PRELIMINARY: PRT: 232 AA.
AC O9CY37:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Adenylate kinase 2.
GN AK2.
OS Mus musculus (Mouse).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
OX NCBI_TaxID=10090;
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-EMBRYONIC LIVER;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shigaoka A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Koehli H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L. M., Staudt R., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombeerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K. F.,
RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
RA Hayshtizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC - SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
 DR EMBL: AK010951; BAB27286.1; -
 DR EMBL: BC008610; AA08610.1; -
 DR HSSP: P08166; IAK2.
 DR MGD: MGI:87978; AK2.
 DR InterPro: IPR000850; Adenylate_kin.
 DR Pfam: PF00406; adenylatekinase; 1.
 DR PRINTS: PRO0094; ADENYLTKINASE.
 DR PRODOM: PD000657; Adenylate_kin; 1.
 DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
 KW kinase; transferase.
 SQ SEQUENCE 232 AA; 25605 MW; EDD60400562323CF CRC64;

Query Match 68.2%; Score 60; DB 11; Length 232;
 Best Local Similarity 66.7%; Pred. No. 0.69;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVINGAPGSGKGT 17
 :|||:|||||
 DB 16 IRAVLGPGGKGT 30

RESULT 15
 Q8R4A6
 ID Q8R4A6 PRELIMINARY; PRT; 130 AA.
 AC Q8R4A6;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE ERA-like protein 1 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Ji Z., Chen S., Liu J., Zhao Z., Chal Y., Liu X., Chen N.;
 RT "Mouse chromosome 11.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF486635; AAM08321.1; -
 FT NON_TER 1
 FT NON_TER 130
 SQ SEQUENCE 130 AA; 13805 MW; 38B0749DAE63C5BB CRC64;

Query Match 65.9%; Score 58; DB 11; Length 130;
 Best Local Similarity 55.6%; Pred. No. 0.73;
 Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLRAVINGAPGSGKGTV 18
 |:|||:|||:|||||
 DB 78 RVLRAVVLGAPNCKSTL 95

Search completed: April 24, 2003, 10:18:17
 Job time : 32 secs

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